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THE POISSON PASCAL DISTRIBUTION[1]

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1. INTRODUCTION

Elementary distributions such as the Poisson, the Logarithmic and the Binomial which can be formulated on the basis of simple models have been found to be inadequate to describe the situations which occur in a number of phenomena. The Neyman Type A (cf. Evans [5]), the Negative Binomial (cf. Bliss and Fisher [3]), and the Poisson Binomial (cf. McGuire *et al.* [8]), which combine two of the elementary distributions through the processes of compounding and generalizing (cf. Gurland [7]), have been fitted with varying degrees of success to data from a number of biological populations. The aim of this paper is to study what may be called the Poisson Pascal distribution which includes the Neyman Type A and Negative Binomial as particular limiting cases and serves as a natural complement of the Poisson Binomial.

2. FORMULATION OF POISSON PASCAL DISTRIBUTION:

Consider the well-known example of the egg masses and the larvae illustrating the process of generalizing (cf. Neyman [9]). Suppose that the egg masses in a field have a Poisson distribution with probability generating function (p.g.f) exp. $\{\lambda(z - 1)\}$ and that the survivors within an egg mass have a Pascal[4] distribution with p.g.f. $(q - pz)^{-k}$, $p > 0$, $q = 1 + p$, $k > 0$. For the sake of references, we note that, if $g(z)$ is the p.g.f. of a distribution, then the coefficient of z^x in the Taylor's expansion of $g(z)$ yields the probability of count x. Then, by following the arguments in Gurland [7], we obtain for the distribution of the survivors in the field, the Poisson Pascal distribution with p.g.f.

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[1]This research was sponsored in part by the Air Force Office of Scientific Research.

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[3]On leave at Mathematics Research Center, U. S. Army, University of Wisconsin.

[4]Feller [6] refers to the distribution with p.g.f. $(q - pz)^{-k}$, $p > 0$, $q = 1 + p$, $k = 1, 2, 3 \cdots$ etc. However, we will use the work Pascal as synonymous with Negative Binomial and use it in the place of the latter since it is shorter.

$$\exp\{\lambda[(q - pz)^{-k} - 1]\}, \quad \lambda > 0, \quad k > 0, \quad p > 0, \quad q = 1 + p. \qquad (1)$$

It is believed that most of the deviation of the distribution of the survivors from the simple distributions mentioned above stems from (i) the complex structure of survivors within an egg mass and (ii) the movement of survivors from place to place. Since the Negative Binomial distribution has been found to be very useful in fitting data involving this type of heterogeneity, it is reasonable to suppose that the Poisson Pascal will give a better description of the population of the survivors in a field.

The Poisson Pascal distribution can also be looked upon as the result of compounding a Pascal distribution with p.g.f. $(q - pz)^{-k_1}$ by taking k_1 to behave as kx where k is a positive constant and x a Poisson random variable with p.g.f. $\exp\{\lambda(z - 1)\}$.

3. SOME PROPERTIES OF THE POISSON PASCAL DISTRIBUTION

The limiting forms that the Poisson Pascal distribution takes as the parameters take on extreme values are given in Table 1. It is to be

TABLE 1

SOME LIMITING FORMS OF THE POISSON PASCAL DISTRIBUTION

No.	Limits Taken	Name and p.g.f. of the limit
1	$k \to \infty, p \to 0$ $pk = \lambda_1$	Neyman Type A, $\exp\{\lambda[\exp(\lambda_1(z - 1) - 1]\}$
2	$k \to 0, \lambda \to \infty$ $\lambda k = k_1$	Negative Binomial, $(q - pz)^{-k_1}$
3	$p \to 0, \lambda \to \infty$ $\lambda kp = \lambda_1$	Poisson, $\exp\{\lambda_1(z - 1)\}$

noted that the Neyman Type A and the Pascal distributions are among the limiting forms.

The flexibility of the Poisson Pascal was compared quantitatively with that of the Neyman Types A, B, C, Pascal, and Poisson Binomial by evaluating the relative skewness and kurtosis of each for fixed mean k_1p_1 and variance $k_1p_1(1 + p_1)$ using the indices $\kappa_{[3]}/k_1p_1^3$ and $\kappa_{[4]}/k_1p_1^4$ respectively along the lines of Anscombe [1]. The range of numerical values of these indices for each of the foregoing distributions is shown in Table 2. It is apparent that the Poisson Pascal covers the entire range of distributions from Neyman Type A to Pascal with respect to skewness and kurtosis. Also, the ranges of these ratios for

TABLE 2

COMPARISON OF SKEWNESS AND KURTOSIS OF CERTAIN DISTRIBUTIONS

No.	Name	Range of Skewness	Range of Kurtosis
1	Neyman Type A	1	1
2	Neyman Type B	9/8	27/20
3	Neyman Type C	6/5	8/5
4	Pascal	2	6
5	Poisson Pascal	(1,2)	(1,6)
6	Poisson Binomial	(0,1)	(0,1)

the Poisson Pascal and the Poisson Binomial are disjoint. Since their p.g.f.s have the common form

$$\exp\{\lambda[(q - pz)^{-k} - 1]\}, \tag{2}$$

we observe that the distribution with (2) for p.g.f. wherein $\lambda > 0$, $q = 1 + p$, $p > 0$ when $k > 0$ and $-1 < p < 0$ when k is a negative integer, covers a very wide range of distributions. As an aid in computing the values of the ratios for the samples to obtain an idea as to how close the sample distribution is to the various distributions mentioned in Table 2, formulae to compute the factorial cummulants $\kappa_{[i]}$ using sample moments are given in Appendix A.

Since the first two frequencies were large in the sets of data to which this (and similar) distributions were fitted, the ratio of the first two frequencies were compared for some of these distributions. It can be easily shown that the value of this ratio for the Poisson Pascal distribution lies between the ratios for the Neyman Type A and the Pascal distributions. The ratios are given for brevity in Table 3.

TABLE 3

COMPARISON OF THE RATIO OF THE FIRST TWO FREQUENCIES WITH MEAN AND VARIANCE FIXED AS k_1P_1 AND $k_1P_1(1 + p_1)$

No.	Distribution	Ratio of Frequencies
1	Neyman Type A	$k_1p_1 \exp(-p_1)$
2	Neyman Type B	$2k_1\{1 - \exp(-3p_1)(1 + 3p_1)\}/(p_1q_1)$
3	Neyman Type C	$3k_1\{2p_1 \exp(-4p_1) + 2[-2 \exp(-4p_1) + 64p_1^2 + 4p_1]\}/4p_1^3$
4	Pascal	$k_1p_1(1 + p_1)^{-1}$
5	Poisson Pascal	$k_1p_1(1 + p_1)/(k + 1)^{-k-1}$

4. FITTING POISSON PASCAL AND EFFICIENCY OF METHODS OF ESTIMATION

Since obtaining maximum likelihood estimates is very cumbersome, *ad hoc* methods were used to estimate the parameters. When the mean and the variance were large, use was made of the method of the first three moments. When they were moderate and the proportion of the zero frequency large, use was made of the method of the first two moments and the proportion of the zero frequency. When the first two frequencies were large in comparison with the remaining, the method of the first two moments and the ratio of the first two frequencies was used in estimation. The equations for estimation are given in Appencix C. The fit of this distribution to the data of Beall and Rescia [2] are given in Tables 4 and 5. For the sake of reference, the fit of a generalization of the Neyman Type A as given by the authors of these data are also given alongside. The relatively good fit of the Poisson Pascal is apparent.

For obtaining a comparison of the various methods of estimation, it was decided to compute the efficiency function

TABLE 4

FIT OF THE OBSERVED FREQUENCY OF LESPEDEZA CAPITATA, TABLE V OF [2]

Plants	Observed Frequency	Expected frequency due to Poisson Pascal (Method of Moments)	Expected frequency as in [2]
0	7178	7185.0	7217.6
1	286	276.0	218.6
2	93	94.5	105.5
3	40	41.5	50.9
4	24	20.2	24.5
5	7	10.4	11.8
6	5	5.6	5.7
7	1	3.1	2.8
8	2	1.7	1.3
9	1	1.0	.6
10	2	.6	.3
11+	1	.3	.4
χ^2	—	9.58	42.97
Degrees of Freedom	—	8	9

E = 1/(Generalized variance × Information determinant) (cf. Cramer [4], pp. 489–497). (3)

If we denote the parameter vector (λ, p, k) by $(\lambda_1, \lambda_2, \lambda_3)$ and the set of statistics used by (t_1, t_2, t_3), we get the expression for the generalized variance of the estimates as

TABLE 5

FIT OF OBSERVED FREQUENCY OF LEPTINOTARSA DECEMLINEATA, TABLE III OF [2]

Insects	Observed	Expected frequency due to Poisson Pascal, (method of two moments and first frequency	Expected frequency as in [2]
0	33	33.0	39.5
1	12	9.8	6.0
2	5	7.4	4.9
3	6	5.5	3.4
4	5	4.0	3.2
5	0	2.9	2.5
6	2	2.1	2.0
7	2	1.5	1.6
8	2	1.1	1.3
9	0	.8	1.0
10	1	.6	.8
11+	2	1.3	3.3
χ^2	—	6.88	13.75
Degrees of Freedom	—	8	9

$$G = |V(t_1,t_2,t_3)| \Big/ \left|\frac{\partial(\tau_1, \tau_2, \tau_3)}{\partial(\lambda_1, y_2, \lambda_3)}\right|^2, \quad (4)$$

where τ_1, τ_2, τ_3 are the functions of λ_1, λ_2 and λ_3 estimated consistently by t_1, t_2, t_3. A proof of this is given in Appendix B. Since evaluating the covariance matrix $V(t_1, t_2, t_3)$ and the derivatives of t_1, t_2 and t_3 follows from the regular statistical techniques, no elaboration need be made here. A formula for the information determinant (cf. Shenton [10]) is

$$n^3 I = \begin{vmatrix} \sum_x \frac{1}{P_x}\frac{\partial P_x}{\partial \lambda_1}\frac{\partial P_x}{\partial \lambda_1} & \sum_x \frac{1}{P_x}\frac{\partial P_x}{\partial \lambda_1}\frac{\partial P_x}{\partial \lambda_2} & \sum_x \frac{1}{P_x}\frac{\partial P_x}{\partial \lambda_1}\frac{\partial P_x}{\partial \lambda_3} \\ \sum_x \frac{1}{P_x}\frac{\partial P_x}{\partial \lambda_2}\frac{\partial P_x}{\partial \lambda_1} & \sum_x \frac{1}{P_x}\frac{\partial P_x}{\partial \lambda_2}\frac{\partial P_x}{\partial \lambda_2} & \sum_x \frac{1}{P_x}\frac{\partial P_x}{\partial \lambda_2}\frac{\partial P_x}{\partial \lambda_3} \\ \sum_x \frac{1}{P_x}\frac{\partial P_x}{\partial \lambda_3}\frac{\partial P_x}{\partial \lambda_1} & \sum_x \frac{1}{P_x}\frac{\partial P_x}{\partial \lambda_3}\frac{\partial P_x}{\partial \lambda_2} & \sum_x \frac{1}{P_x}\frac{\partial P_x}{\partial \lambda_3}\frac{\partial P_x}{\partial \lambda_3} \end{vmatrix}. \quad (5)$$

The principal problems in evaluating I for a value of (λ, p, k) therefore are (i) to evaluate the various P_x and the derivatives of P_x and (ii) to determine the number of terms to be used in summing the infinite series. To obtain P_x, let

$$g(z) = \exp\{\lambda[(q - pz)^{-k} - 1]\} \quad (6)$$

and

$$h(z) = (q - pz)^{-k}.$$

By differentiating (6) successively we get

$$g'(z) = \lambda g(z)h'(z), \quad (7)$$

and

$$g^{(x+1)}(z) = \lambda \sum_{i=0}^{x} \binom{x+1}{i} g^{(i)}(z)h^{(x+1-i)}(z). \quad (8)$$

Set $z = 0$ in equations (6), (7) and (8) and observe that $g^{(x)}(0) = x!\,P_x$ and $h^{(x)}(0) = x!\,\pi_x$ where

$$\pi_x = \frac{(k + x - 1)!}{(k - 1)!\,x!} p^x q^{-k-x}, \quad (9)$$

is the probability of x in the Pascal distribution with $h(z)$ as p.g.f. Then we have the recurrence formulae

$$P_0 = \exp.\{\lambda[(q)^{-k} - 1]\} \quad (10)$$

and

$$P_{x+1} = \frac{\lambda}{x+1}\left\{\sum_{i=0}^{x}(x + 1 - i)\pi_{x+1} - i\,P_i\right\}, \quad (11)$$

which can be repeatedly used to evaluate any P_x.

The various derivative are given by

$$\frac{\partial P_x}{\partial \lambda_1} = \frac{\partial P_x}{\partial \lambda} = \left\{\frac{\partial^x}{\partial z^x}\left[\frac{\partial g(z)}{\partial \lambda}\right]\right\}_{z=0} = \frac{1}{x!}\left\{\frac{\partial^x}{\partial z^x}[g(z)(h(z) - 1)]\right\}_{z=0}$$

$$= \frac{q}{\lambda k p}(x + 1)P_{x+1} - P_x\left(1 + \frac{r}{\lambda k}\right), \quad (12)$$

$$\frac{\partial P_x}{\partial \lambda_2} = \frac{\partial P_x}{\partial p} = \frac{1}{x!}\left\{\frac{\partial^x}{\partial z^x}\left[\frac{\partial}{\partial P}\, g(z)\right]\right\}_{z=0} = \frac{1}{x!}\left\{\frac{\partial^x}{\partial z^x}\left[\frac{z}{p}\, g'(z)\right]\right\}_{z=0}$$

$$= \frac{1}{p}\{xP_x - (x+1)P_{x+1}\} \qquad (13)$$

and

$$\frac{\partial P_x}{\partial \lambda_3} = \frac{\partial P_x}{\partial k} = \frac{1}{x!}\left\{\frac{\partial^x}{\partial z^x}\left[\frac{\partial}{\partial r}\, g(z)\right]\right\}_{z=0}$$

$$= \frac{1}{x!}\left\{\frac{\partial^x}{\partial z^x}\left[-\lambda g(z)h(z)\,\log\,(q - pz)\right]\right\}_{z=0}$$

$$= \frac{1}{kp}\sum_{i=1}^{x}(p/q)^i\,\frac{1}{i}\,\{q(x - i + 1)P_{x-i+1} - p(x - i)P_{x-i}\}$$

$$- \frac{1}{kp}\,(\log q)\{q(x+1)P_{x+1} - pxP_x\} \qquad (14)$$

for all x.

TABLE 6

EFFICIENCY OF THE METHOD OF THE FIRST THREE MOMENTS FOR THE POISSON PASCAL

λ	p	k .1	.3	.5	1.0	2.0
.1	.1	.84	.82	.82	.81	.76
.1	.3	.59	.58	.58	.54	.47
.1	.5	.45	.44	.43	.40	.33
.1	1.0	.26	.25	.24	.22	.18
.1	2.0	.13	.12	.12	.12	.13
.5	.1	.90	.81	.82	.77	.67
.5	.3	.59	.58	.56	.49	.35
.5	.5	.46	.44	.41	.34	.22
.5	1.0	.26	.25	.23	.18	.10
.5	2.0	.13	.13	.12	—	—
1.0	.1	.81	.83	.82	.75	.63
1.0	.3	.59	.59	.55	.46	.28
1.0	.5	.46	.44	.40	.31	.15
1.0	1.0	.27	.25	.23	.15	.05
1.0	—	—	—	—	—	—
5.0	.1	.94*	.99*	.78*	.58*	.21*
5.0	.3	.62*	.56*	.41*	.11*	.01*
5.0	.5	.48*	.38*	.20*	.04*	.00*
5.0	1.0	.29*	.17*	.06*	.02*	.00*
5.0	—	—	—	—	—	—

To determine the number of terms we use the following rule:

Let $T_{ij}(n)$ denote the $(n + 1)$th term in the series involved in the (i, j)th term of matrix (5). Let $S_{ij}(n) = \sum_{r=0}^{n} T_{ij}(r)$. Compute $S_{ij}(n)$ and $\sum_{ij} T_{ij}^2(n)/S_{ij}^2(n)$ for $n = 1, 2, \cdots$ *et cetera* successively till a value of n is reached for which

$$\sum_{ij} T_{ij}^2(n)/S_{ij}^2(n) < 10^{-8}. \tag{15}$$

It is clear from (15) that $| T_{ij}(n) |/| S_{ij}(n) | < 10^{-4}$ for each i and j. If the series converge faster than a geometric series with common ratio less than 0.9 and this convergence starts before the value of n is reached for which (15) is satisfied, the calculated efficiency will be correct to three significant figures. If the significant figures do not cancel out, this should yield the efficiencies computed therefrom, correct to three decimal places. When the inequality (15) was not satisfied for values of $n \leq 20$, the partial sum of the first twenty terms was taken as the value of the series since evaluating the terms of the series

TABLE 7

EFFICIENCY OF THE METHOD OF THE FIRST TWO MOMENTS AND THE FIRST FREQUENCY FOR THE POISSON PASCAL DISTRIBUTION AT $\lambda = 0.1$

		k				
λ	p	.1	.3	.5	1.0	2.0
.1	.1	.99	.98	.98	.98	.98
.1	.3	.93	.94	.95	.94	.93
.1	.5	.90	.90	.91	.91	.89
.1	1.0	.82	.83	.84	.84	.83
.1	2.0	.74	.76	.78	.84	.78
.5	.1	1.00	1.00	.98	.96	.95
.5	.3	.93	.94	.93	.92	.87
.5	.5	.91	.91	.90	.89	.82
.5	1.0	.83	.85	.85	.82	.73
.5	2.0	.75	.78	.81	—	—
1.0	.1	1.00	.99	.97	.96	.94
1.0	.3	.94	.96	.94	.93	.87
1.0	.5	.92	.92	.91	.98	.81
1.0	1.0	.84	.85	.86	.82	.72
1.0	2.0	.88*	.87*	.87*	.87*	.83*
5.0	.1	—	—	.99*	.89*	.98*
5.0	.3	.97*	.99*	1.00*	1.00*	.98*
5.0	.5	.95*	.97*	.98*	.99*	.96*
5.0	1.0	.90*	.96*	.97*	—	—
5.0	2.0	.89*	—	—	—	—

for n larger than 20 is very time consuming. The efficiency when n was restricted to 20 is marked with an asterisk to indicate that they are less likely to be correct to three decimal places. When the efficiency so computed was larger than one (due to the inaccuracy in computing the information determinant), the corresponding cell in the efficiency table is left blank.

The efficiency of the method of moments is given for certain values of (λ, p, k) in Table 6. The efficiency of the method of the first two moments and the first frequency is given in Table 7 and that of the method of the first two moments and the ratio of the first two frequencies in Table 8 for the same values of (λ, p, k).

It is apparent that the method of the first two moments and the ratio of the first two frequencies has high efficiency and is superior to the other two methods when λ is small (and consequently the first two counts account for a large proportion of the observed frequencies). Also the method of the first two moments and the first frequency is highly efficient when λ is moderately large. When λ, p or k approaches

TABLE 8

EFFICIENCY OF THE METHOD OF THE FIRST TWO MOMENTS AND THE RATIO OF THE FIRST TWO FREQUENCIES FOR THE POISSON PASCAL AT $\lambda = 0.1$

λ	p	k = .1	.3	.5	1.0	2.0
.1	.1	1.00	1.00	1.00	1.00	1.00
.1	.3	.98	.99	.99	.99	.98
.1	.5	.99	.98	.98	.97	.94
.1	1.0	.94	.94	.93	.91	.83
.1	2.0	.87	.88	.89	.91	.99
.5	.1	1.00	.99	1.00*	1.00	.99
.5	.3	.98	1.00	.99	.98	.96
.5	1.0	.99	.98	.97	.96	.92
.5	2.0	.94	.94	.93	.89*	.80*
1.0	.1	.98	1.00	1.00	1.00	.99
1.0	.3	.99	1.00	.99	.99	.95
1.0	.5	1.00	.99	.98	.96	.91
1.0	1.0	.95	.94	.93	.88	.79
1.0	2.0	.88*	.89*	.91*	—	—
5.0	.1	—	—	.99*	.95*	.91*
5.0	.3	1.00	.99*	.98*	.89*	.76*
5.0	.5	1.00	.96*	.91*	.80*	.65*
5.0	1.0	.95*	.88*	.79*	.84*	1.00*
5.0	2.0	.90*	.98*	—	—	—

infinity, it can be shown by calculus that the method of moments is much superior to the other two but since the efficiency of each of these methods tends to zero for such values, this has little significance.

5. CONCLUSIONS

On the basis of the properties discussed in Section 3 and the fitting in Section 4, we observe that the Poisson Pascal distribution acts as a bridge between the Neyman Type A and the Negative Binomial distributions and may be used with advantage when the latter distributions are inadequate to represent the population accurately.

From the tables of efficiency, it is clear that in the region of tabulations, at least one of the *ad hoc* methods of estimation suggested above has high efficiency. It is believed that in practice, (λ, p, k) will not be far beyond the region of tabulation and that one of these methods can be used without too much loss of information. Techniques for choosing one of the many *ad hoc* methods on the basis of the sample will be discussed in a future paper.

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APPENDIX

A. Formulae to compute factorial cumulants using moments about the origin:

We first obtain formulae to compute the first four factorial moments $\mu_{(i)}$, $i = 1, \cdots, 4$ using moments about the origin μ_i and then obtain

formulae to evaluate the first four factorial cumulants $\kappa_{[i]}$ $i = 1, \cdots, 4$ using these factorial moments.

As for the first objective we note that $\mu_{[i]} = E\{x(x-1)\cdots(x-i+1)\}$, $i = 1, 2, \cdots$. By expanding the product within the expectation sign and using the elementary properties of the expectation operator, we get

$$\mu_{[1]} = \mu_1' , \qquad \mu_{[2]} = \mu_2' - \mu_1' , \qquad \mu_{[3]} = \mu_3' - 3\mu_2' + 2\mu_1' ,$$

and

$$\mu_{[4]} = \mu_4' - 6\mu_3' + 11\mu_2' - 6\mu_1' . \tag{16}$$

As for the latter, we observe that if $u(t)$ and $\psi(t)$ denote the factorial moment generating function and the factorial cumulant generating function, then $\psi(t) = \log u(t)$. On differentiating the equation successively with respect to t at $t = 0$ and noting that $\kappa_{[i]} = \psi^{(i)}(0)$, we have

$$\kappa_{[1]} = \mu_{[1]} , \qquad \kappa_{[2]} = \mu_{[2]} - \mu_{[1]}^2 ,$$
$$\kappa_{[3]} = \mu_{[3]} - 3\mu_{[1]}\mu_{[2]} + 2\mu_{[1]}^3 ,$$

and

$$\kappa_{[4]} = \mu_{[4]} - 3\mu_{[2]}^2 - 4\mu_{[1]}\mu_{[3]} + 12\mu_{[1]}^2\mu_{[2]} - 6\mu_{[1]}^4 . \tag{17}$$

B. To prove formula (4):

Since τ_1 , τ_2 , τ_3 are functions of λ_1 , λ_2 and λ_3, let us write them more explicitly as $\tau_1(\lambda_1 , \lambda_2 , \lambda_3)$, $\tau_2(\lambda_1 , \lambda_2 , \lambda_3)$ and $\tau_3 (\lambda_1, \lambda_2 , \lambda_3)$ respectively. If $\hat{\lambda}_1 , \hat{\lambda}_2 , \hat{\lambda}_3$ are the estimates of $\lambda_1 , \lambda_2 , \lambda_3$, then using the statistics t_1 , t_2 , t_3 which estimate the τ's consistently, we have

$$t_i = \tau_i(\hat{\lambda}_1 , \hat{\lambda}_2 , \hat{\lambda}_3), \qquad i = 1, 2, 3.$$

Hence, we have the asymptotic relations

$$t_i - \tau_i = \left(\frac{\partial \tau_i}{\partial \lambda_1} , \frac{\partial \tau_i}{\partial \lambda_2} , \frac{\partial \tau_i}{\partial \lambda_3}\right)(\hat{\lambda}_1 - \lambda_1 , \hat{\lambda}_2 - \lambda_2 , \hat{\lambda}_3 - \lambda_3)', \quad i = 1, 2, 3.$$

which can be rewritten as

$$\begin{bmatrix} \hat{\lambda}_1 - \lambda_1 \\ \hat{\lambda}_2 - \lambda_2 \\ \hat{\lambda}_3 - \lambda_3 \end{bmatrix} = \left[\frac{\partial(\tau_1 , \tau_2 , \tau_3)}{\partial(\lambda_1 , \lambda_2 , \lambda_3)}\right]^{-1} \begin{bmatrix} t_1 - \tau_1 \\ t_2 - \tau_2 \\ t_3 - \tau_3 \end{bmatrix}.$$

The generalized variance G of $\hat{\lambda}_1 , \hat{\lambda}_2 , \hat{\lambda}_3$ is then given by

$$G = | E(\lambda_1 - \lambda_1 , \lambda_2 - \lambda_2 , \lambda_3 - \lambda_3)'(\hat{\lambda}_1 - \lambda_1 , \hat{\lambda}_2 - \lambda_2 , \hat{\lambda}_3 - \lambda_3) |$$
$$= | V(t_1 , t_2 , t_3) | \Big/ \left| \frac{\partial(\tau_1 , \tau_2 , \tau_3)}{\partial(\lambda_1 , \lambda_2 , \lambda_3)} \right|^2$$

which is formula (4).

C. Equations for estimation:

We give below the equations for estimating the parameters for the various methods mentioned in Section 4. Their derivations are omitted for brevity.

i. Equations for the estimation of parameters using the first three moments are:

$$k = \frac{\hat{\kappa}_{[3]}\hat{\kappa}_{[1]}}{\hat{\kappa}_{[3]}\hat{\kappa}_{[1]} - (\hat{\kappa}_{[2]})^2} - 2, \tag{18}$$

$$p = \hat{\kappa}_{[2]}/(\hat{\kappa}_{[1]}(k+1)), \tag{19}$$

$$\lambda = \hat{\kappa}_{[1]}/(kp). \tag{20}$$

ii. Equations for the estimation of parameters using the first two moments and the proportion $\hat{P}_0$ of zeros are:

$$p \log\left\{1 + \left(\frac{\hat{\kappa}_{[2]}}{\hat{\kappa}_{[1]}} - p\right)\frac{\log \hat{P}_0}{\hat{\kappa}_{[1]}}\right\} + \left(\frac{\hat{\kappa}_{[2]}}{\hat{\kappa}_{[1]}} - p\right)\log(1+p), \tag{21}$$

$$k = \frac{\hat{\kappa}_{[2]}}{p\hat{\kappa}_{[1]}} - 1, \qquad \lambda = \hat{\kappa}_{[1]}/(kp). \tag{22}$$

iii. Equation for the estimation of the parameter p using the first two moments and the ratio $\hat{P}_1/\hat{P}_0$ of the first two frequencies is

$$\frac{\log(1+p)}{p} = \frac{\hat{\kappa}_{[1]}}{\hat{\kappa}_{[2]}} \log\{\hat{\kappa}_{[1]}\hat{P}_0/\hat{P}_1\}. \tag{24}$$

k and λ are then estimated by using equations (22) and (23).

SOME RANK SUM MULTIPLE COMPARISONS TESTS

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1. SUMMARY

Rank sum tests for multiple comparisons and suitable to the completely random design with equal sample sizes are discussed. Significance tables and some facts about the joint distribution of rank sums are given. An example illustrating test procedures and making use of the tables is presented.

2. INTRODUCTION

A number of nonparametric tests based on ranks have been proposed for the comparison of treatments in a completely random design. For example, we have the Wilcoxon-Mann-Whitney test [21, 10], basically a two-sample test with a per-comparison error rate.

Also, Kruskal and Wallis [9] have proposed a rank test which is an analogue of Snedecor's F-test. This test provides evidence concerning the presence of real differences but is of limited use in locating them.

Steel [16, 17] has presented rank tests for comparing treatments against control and for all pairwise comparisons. Both of these tests use experiment-wise error rates.

Pfanzagl [13], as part of a more general theory, has discussed a two-step nonparametric decision process based on ranks, for testing the null hypothesis that k samples come from the same population and, if this is rejected, for deciding which one of the samples comes from a different population. No tables are given but it is suggested that they might be obtained by random sampling. It is also shown that the limiting distribution of the multivariate criterion is multinormal.

The per-comparison error rate test is sometimes criticized, particularly when all possible paired comparisons are made, because it will almost certainly lead to false declarations of significance when the experiment includes many treatments and if customary significance levels are used. It is also deemed inappropriate when the experiment is considered to be the conceptual unit.

The experimentwise error rate test is sometimes criticized because it

requires such a large difference to be declared significant that it becomes difficult to detect any but the largest real differences when customary significance levels are used. Also, it may be that the individual comparison is considered to be the conceptual unit.

A brief discussion of these error rates is given by Steel [18] in response to *Biometrics* Query 163.

Choice of a definition of error rate in the conduct of a particular experiment seems somewhat less crucial when it is realized that we can compute the significance level for a particular definition of error rate from knowledge of the chosen significance level for any other definition of error rate. This is not generally a simple computation unless the comparisons are independent. In the case of p independent comparisons, if α' and α are the experimentwise and per-comparison error rates respectively, we have the relation: $1 - \alpha' = (1 - \alpha)^p$.

When comparisons are not independent, computation of comparable significance levels for different definitions of error rate depends upon the extent of the dependence and the nature of the multiple comparisons test. No individual is likely to perform such a computation for a single experiment. Thus a table needs to be prepared for comparing the customary significance levels for differently defined error rates. For tests based on an underlying normal distribution, this has been done fairly extensively by Harter [4, 6].

The experimenter may try to meet the usual criticisms of per-comparison and experimentwise error rates by choice of a non-standard significance level or an alternative test procedure. Presently, tables of significant values for such levels do not appear to be available for experimentwise error rates; in the case of alternative tests, several are available, including the Newman-Keuls [11, 7] procedure and Duncan's [1,5] new multiple range test, which are sequential in nature.

This paper is concerned with rank tests, in particular with tables for an all-pairs-of-treatments test with an experimentwise error rate, and the use of these tables for a fixed rank sum test, an analogue of Tukey's w-procedure (for example, see Steel and Torrie [19]), and for two multiple rank sum tests, analogues of the Newman-Keuls procedure and of Duncan's test. Table 2 is used in the first two cases, Table 3 in the last case.

3. CONSTRUCTION OF TABLES

The proposed tests call for rank sums and their conjugates computed for all pairwise comparisons of treatments. The minimum of each rank sum and conjugate is used, the set of minima providing a multivariate rank sum test criterion. These sums are compared with a single

tabulated value for the fixed rank sum test and with several values for the multiple rank sum tests. Table 2 provides critical values for the analogues of Tukey's and the Newman-Keuls tests; Table 3 provides for the analogue of Duncan's test.

Methods for constructing probability tables and limited tables have been presented earlier [16, 17]. Construction of exact tables of any extent was beyond the computing facilities available. However, some machine time was available and this was used for some sampling experiments.

It was originally intended to ignore the discrete nature of the data and to use the Kolmogorov-Smirnov [8, 14] one-sample test to determine the sample size necessary to attain a certain precision in the constructed tables. However, available computing facilities limited sampling to values of $k = 3$ and 4 (2 and 3 treatments when one was control) and $n = 4$ (1) 10. In addition, samples were obtained for $k = 5$, $n = 4$, 5 and $k = 6$, $n = 5$. The number of permutations obtained for each case was either 5000 or 6000. These tables were used only for checking purposes against the few exact distributions available, $k = 3$ and $n = 3$ (1) 6, and against approximations used in constructing these and earlier tables.

It was assumed that the various multivariate rank sum criteria are distributed approximately as multinormal distributions having mean vectors and variance-covariance matrices as given in the appendix. (Fraser's [3] vector form of the Wald-Wolfowitz-Hoeffding theorem does not apply since the $|| C_{na}(i, j) ||$'s of Fraser do not exist for the test criteria used here.)

On this assumption, one naturally proceeds to base computation on presently available tables. Tables for Tukey's and Duncan's tests are the obvious choice for all-pairs tests. These tests are based on a multinormal distribution with $\rho^2 = n_i n_j/(n_k + n_i)(n_k + n_j)$ where the present distribution calls for $\rho^2 = n_i n_j/(n_k + n_i + 1)(n_k + n_j + 1)$, a small difference. The appropriate tables are, then, tables of the Studentized range with known variance, that is, infinite degrees of freedom. Table 22 of Pearson and Hartley [12] is such a table, gives percentage points of .10, .05 and .01, is appropriate for the first two tests, and was used in computing Table 2. Corrected tables for Duncan's test have been computed by Harter [5] and this table was used in computing Table 3, also for percentage points of .10, .05 and .01.

Table 2 was constructed by taking the integral part of $\mu - t\sigma/\sqrt{2}$, unless the decimal fraction was $> .9$, in which case the next higher integer was tabulated, where t was obtained from the distribution of w/σ, w = range, Table 22 of Pearson and Hartley [12]. Since rank

sums are essentially differences, it is necessary to introduce $\sqrt{2}$ into the denominator as shown. Tabulated rank sum values for $\alpha = .10$ differed in only two cases from values obtained by sampling. In particular, for $k = 4$, $n = 4$, no value is significant by sampling; for $k = 3$, $n = 6$, a rank sum of 25 is significant by sampling whereas 26 is not. Values for $\alpha = .05$ differed in no case. Values for $\alpha = .01$ ran lower than those obtained by sampling, the difference increasing with n to a value of two in three cases. Hence, it is reasonable to conclude that tabulated values of the rank sum are conservative (low) for $\alpha = .01$.

The first attempt to construct Table 3 led to values which tended to run high for $\alpha = .10$, correct for $\alpha = .05$, and low for $\alpha = .01$, relative to values found by sampling. For this reason, tabulated values are of $\mu - t\sigma/\sqrt{2}$ decreased by unity for $\alpha = .10$, as computed for $\alpha = .05$, and increased by unity for $\alpha = .01$. On this basis, tabulated values for $\alpha = .10$ appear to be low, hence conservative, when not in agreement with sampling results; in particular, 7 out of 19 tabulated values are one unit low. For $\alpha = .05$, 3 out of 19 values are one unit high. For $\alpha = .01$, 5 out of 19 values are one unit low, with three of these being for $n = 5$.

Tables have already been constructed [16], using Dunnett's [2] tables, for the treatments against control test. These tables agree well with the sampling results. In no case is there a difference of more than one in the value of the test criterion, with the tables most often giving the conservative (lower) value.

TABLE 1

FINAL WEIGHTS OF CHICKS AT SIX WEEKS (GRAMS) FOR VARIOUS SOURCES OF PROTEIN SUPPLEMENT

H Horse-bean	*L* Linseed Oil Meal	*Sb* Soybean Oil Meal	*Sf* Sunflower Seed Oil Meal	*M* Meat Meal	*C* Casein
179	309	243	423	325	368
160	229	230	340	257	390
136	181	248	392	303	379
227	141	327	339	315	260
217	260	329	341	380	404
168	203	250	226	153	318
108	148	193	320	263	352
124	169	271	295	242	359
143	213	316	334	206	216
140	257	267	322	344	222

4. USE OF TABLES

To illustrate the use of the tables, the data in Query 60 of *Biometrics* (15) are used. These are presented in Table 1. Since the test is presently unavailable for unequal sample sizes, only the first ten items in each treatment are used.

The following set of minimum rank sums is obtained by pairwise rankings, a minimum being the lesser of the rank sum T, and its conjugate, $T' = (2n + 1)n - T$; minimum treatment is the treatment for which the rank sum is minimum. Ties were assigned their average rank. This gives a multivariate criterion with 15 entries.

Comparison	*H, Sf*	*H, Sb*	*H, C*	*L, Sf*	*H, M*	*L, C*
Minimum Rank Sum	56	57	58	60	62	64½
Minimum Treatment	H	H	H	L	H	L

Comparison	*Sb, Sf*	*H, L*	*L, Sb*	*L, M*	*Sb, C*	*Sf, M*	*M, C*	*Sb, M*	*Sf, C*
Minimum Rank Sum	71	75	75	75½	80	82	84	100	103
Minimum Treatment	*Sb*	*H*	*L*	*L*	*Sb*	*Sf*	*M*	*Sb*	*Sf*

From Table 2, a rank sum of 67 is significant at the 5 percent level, $k = 6$, $n = 10$; hence six comparisons are declared significant.

The device, used with multiple comparisons procedures, of underlining treatments which cannot be distinguished by their means may be adapted to apply to rank sum procedures. Thus, from the test, it appears that *H* and *L*, and *L*, *Sb*, *M*, *Sf* and *C* form two groups as a first step; since *L* can be distinguished from *Sf* and *C*, the latter group becomes two, namely *L*, *Sb* and *M*, and *Sb*, *M*, *Sf* and *C*. We have:

$$\underline{H \quad L} \qquad \underline{Sb \quad M} \qquad \underline{Sf \quad C}$$

Ordering of *Sb* and *M*, and of *Sf* and *C* was done on the basis of rank sums for these paired comparisons though this does not imply that this is the only, or even the best, method.

This procedure is an analogue of Tukey's w-procedure [19]. The significance level is for an experimentwise error rate. Use of Wilcoxon's [21] two-sample test, with its per-comparison error rate, calls for a significant rank sum of 78; this will result in four more comparisons being declared significant.

TABLE 2

PERCENTAGE POINTS OF THE MINIMUM RANK SUM
(AN APPROXIMATION)

Number in treatment	α	k = number of treatments being tested							
		3	4	5	6	7	8	9	10
4	.10	10	10	—	—	—	—	—	—
	.05	—	—	—	—	—	—	—	—
	.01	—	—	—	—	—	—	—	—
5	.10	17	16	15	15	—	—	—	—
	.05	16	15	—	—	—	—	—	—
	.01	—	—	—	—	—	—	—	—
6	.10	26	24	23	22	22	21	21	—
	.05	24	23	22	21	—	—	—	—
	.01	—	—	—	—	—	—	—	—
7	.10	36	34	33	32	31	30	30	29
	.05	34	32	31	30	29	28	28	—
	.01	29	28	—	—	—	—	—	—
8	.10	48	46	44	43	42	41	40	40
	.05	45	43	42	40	40	39	38	38
	.01	40	38	37	36	—	—	—	—
9	.10	62	59	57	56	55	54	53	52
	.05	59	56	54	53	52	51	50	49
	.01	52	50	48	47	46	45	—	—
10	.10	77	74	72	70	69	68	67	66
	.05	74	71	68	67	66	64	63	63
	.01	66	63	62	60	59	58	57	56

It is also possible to propose and carry out a sequential procedure, an analogue of the Newman-Keuls procedure, which uses several rank sums for testing. For this procedure, the above analysis is the first step and has separated the treatments into three groups. To proceed, we assume that declared differences are indeed real. Hence to test H versus L, the first group, we may use Wilcoxon's [21] two-sample test, H and L are declared significantly different and the line beneath them may be removed.

Further, compare L, Sb and M using the critical value for $k = 3$, $n = 10$, namely 74. L versus Sb and L versus M at 75 and $75\frac{1}{2}$ are be-

yond the 10 percent point but are not quite significant. We cannot distinguish among these three treatments.

Finally, consider the group composed of treatments *Sb*, *M*, *Sf* and *C*. The critical value is 71, $k = 4$, $n = 10$. The treatments *Sb* and *Sf* can be distinguished and we must, then, change the order of *Sf* and *C* from that proposed when the fixed rank sum test was used. No further differences will be declared significant by this procedure. We have:

H *L* *Sb* *M* *C* *Sf*

For the Tukey and Newman-Keuls parametric procedures, we find means of 160.2(*H*), 211.0(*L*), 267.4(*Sb*), 278.8(*M*), 323.2(*Sf*) and 326.8(*C*). Also $s_{\bar{x}} = 18.03$ and significant ranges are 51.2, 61.5, 67.6, 71.9 and 75.2 for $k = 2, \cdots, 6$ respectively.

For Tukey's test, the fixed rank sum is 75.2. We find:

H *L* *Sb* *M* *Sf* *C*

For the Newman-Keuls procedure, we find:

H *L* *Sb* *M* *Sf* *C*

We now compare the results obtained from applying the parametric and non-parametric procedures.

The fixed rank sum test and Tukey's test lead to the same conclusions. Both are based on experimentwise error rates.

Conclusions drawn from the multiple rank sum test and the Newman-Keuls test differ as follows. *L* versus *M* is significant by the Newman-Keuls procedure only; *Sb* versus *Sf* is significant by the rank sum test only. Otherwise, the procedures lead to the same conclusions. Fifteen paired tests have been made. Since *L* versus *M* is nearly significant and *Sb* versus *Sf* is just significant by the multiple rank sum test, it would appear that the two methods lead to conlcusions, for this example, that differ only slightly.

The other multiple rank sum test to be considered is an analogue of Duncan's new multiple range test. Table 3 provides critical values. A rank sum of 75 is significant at the 5 percent level, $k = 6$, $n = 10$; hence nine comparisons are significant. Tentatively, we have:

H *L* *M* *Sb* *C* *Sf*

Unfortunately, this includes an anomaly since *Sb* versus *Sf* is also declared significant. The same would be true if the Wilcoxon-Mann-Whitney test were being used at a significance level (between 5 percent and 1 percent) calling for a critical value of 75.

TABLE 3

PERCENTAGE POINTS OF THE MINIMUM RANK SUM FOR DUNCAN ANALOGUE (AN APPROXIMATION)

Number in treatment	α	k = number of treatments being tested							
		3	4	5	6	7	8	9	10
	.10	11	10	10	10	10	10	10	10
4	.05	10	10	10	10	10	10	10	10
	.01	—	—	—	—	—	—	—	—
	.10	18	18	17	17	17	17	17	17
5	.05	17	17	16	16	16	16	16	16
	.01	15	15	15	—	—	—	—	—
	.10	27	26	26	26	26	25	25	25
6	.05	26	25	25	25	25	24	24	24
	.01	23	22	22	22	22	21	21	21
	.10	37	37	37	36	36	36	36	36
7	.05	36	35	35	35	34	34	34	34
	.01	32	32	31	31	30	30	30	30
	.10	50	49	49	49	48	48	48	48
8	.05	48	47	47	46	46	46	46	45
	.01	43	42	42	41	41	41	41	40
	.10	65	64	63	63	62	62	62	62
9	.05	62	61	60	60	60	59	59	59
	.01	56	55	54	54	53	53	53	52
	.10	81	80	79	79	78	78	78	77
10	.05	77	76	76	75	75	74	74	74
	.01	70	69	68	68	67	67	67	66

On the basis that treatments declared significantly different are indeed so, we proceed to test treatments M, Sb, C and Sf using $k = 4$ and L and M using $k = 2$. The final result is:

$$\underline{H \quad L \quad Sb \quad M \quad C \quad Sf}$$

This result is the same as that obtained using the Wilcoxon-Mann-Whitney test.

Using Duncan's (parametric) new multiple range test, we find:

$$\underline{H \quad L \quad Sb \quad M \quad Sf \quad C}$$

Conclusions from Duncan's test and its rank sum analogue differ only in that the parametric test finds *Sb* versus *C* to be significant.

The multiple rank sum test can be adapted to apply to testing treatments versus control as well.

5. APPENDIX—THEORY

The problem is concerned with pairwise testing of treatments in the one-way classification or completely random design.

The test criteria are rank sums, computed as for Wilcoxon's [21] two sample test, for appropriate pairs of treatments. Rank sums will be referred to Tables 2 or 3 for testing rather than to White's [20] table for the Wilcoxon-Mann-Whitney test.

Two tests will be considered:

1. The all pairs test, in detail.
2. Treatments against control, rather briefly.

For the all pairs test, let X_i , $i = 1, \cdots, k$ be random variables measuring some characteristic for each of k samples or treatments. Let there be n_i observations on the i-th treatment. Computation of the test criterion requires us to:

1. Rank the X_i's and the X_j's, all $i < j$, assigning rank 1 to the least observation.
2. Add ranks for the variable with fewer observations to give T_{ij} . (There is no loss of generality if we assume $n_1 \leq n_2 \leq \cdots \leq n_k$).
3. Compute the conjugate of T_{ij} , namely $T'_{ij} = (n_i + n_j + 1)n_i - T_{ij}$.

The conjugate is the rank total that would be obtained if rank 1 were assigned to the highest observation. Conjugates are required for two-tailed tests.

Consider $(T_{12}, \cdots, T_{1k}, T_{23}, \cdots, T_{k-1,k})$, a criterion with $\binom{k}{2}$ components. Rank tests are based on the assumption that, under H_0 , all permutations of the $\sum n_i$ observations are equally likely. Hence, we must know the number of ways in which $(T_{12}, \cdots, T_{k-1,k})$ can be obtained. For this, a recursion formula is given in [14]. This provides a method, though tedious, of deriving the distribution of $(T_{12}, \cdots, T_{k-1,k})$.

The distribution of $(T_{12}, \cdots, T_{k-1,k})$ has been shown to have the following parameters [14]:

$$E(T_{ij}) = \mu_{ij} = n_i(n_i + n_j + 1)/2,$$

$$E(T_{ij} - \mu_{ij})^2 = \sigma^2_{ij} = n_i n_j(n_i + n_j + 1)/12,$$

$$E(T_{ki} - \mu_{ki})(T_{kj} - \mu_{kj}) = \sigma_{ki,kj} = n_k n_i n_j/12 = \sigma_{kj,ij},$$

$$E(T_{ki} - \mu_{ki})(T_{ij} - \mu_{ij}) = \sigma_{ki,ij} = -n_k n_i n_j/12,$$

$$E(T_{gh} - \mu_{gh})(T_{ij} - \mu_{ij}) = \sigma_{gh,ij} = 0,$$
$$\rho^2_{ih,hj} = \rho^2_{ih,jh} = \rho^2_{hi,hj} = n_i n_j/(n_h + n_i + 1)(n_h + n_j + 1),$$
$$\rho^2_{gh,ij} = 0.$$

The determinant of the variance-covariance matrix is:

$$[\prod_i n_i^{k-1}(\sum n_i + 1)^{k-1}]/12^{\binom{k}{2}}.$$

The elements in the inverse of the variance-covariance matrix are: Corresponding to the variance of T_{ij},

$$12(\sum n_\alpha + 1 - n_i - n_j)/n_i n_j(\sum n_\alpha + 1).$$

Corresponding to a covariance with the T's having a common subscript, h, in the same position:

$$-12/n_h(\sum n_\alpha + 1).$$

Corresponding to a covariance with the T's having a common subscript, i, in different positions, for example T_{hi} and T_{ij}:

$$12/n_i(\sum n_\alpha + 1).$$

Finally, the element corresponding to $\sigma_{gh,ij}$ is zero.

The determinant of the variance-covariance matrix may be evaluated as follows: from the ith row of the determinant, factor $n_1 n_{1+i}/12$, $i = 1, \cdots, k-1$; from the $([k-1]+i)$-th row, factor $n_2 n_{2+i}/12$, $i = 1, \cdots, k-2$; $\cdots$; from the last row, factor $n_{k-1}n_k/12$. The product of these factors is $\prod_i n_i^{k-1}/12^{\binom{k}{2}}$.

The entries in the determinant which is the other factor may be described somewhat crudely as follows.

The i-th diagonal block, $i = 1, \cdots, k-1$, which contains the variances and covariances of the T_{ij}'s, fixed i and $j > i$, will be

$$\begin{bmatrix} n_i + n_{i+1} + 1 & n_{i+2} & \cdots & n_k \\ n_{i+1} & n_i + n_{i+2} + 1 & \cdots & n_k \\ \cdots & \cdots & \cdots & \cdots \\ n_{i+1} & n_{i+2} & \cdots & n_i + n_k + 1 \end{bmatrix}.$$

This is a $(k-i) \times (k-i)$ block.

The block consisting of the same rows and the first $(k-1)$ columns is

$$\begin{bmatrix} 0 & \cdots & 0 & -n_1 & n_1 & 0 & 0 & \cdots & 0 \\ 0 & \cdots & 0 & -n_1 & 0 & n_1 & 0 & \cdots & 0 \\ \cdots & & & \cdots & & & \cdots & & \\ \underbrace{0 \quad \cdots \quad 0}_{i-2 \text{ columns}} & & & -n_1 & \underbrace{0 \quad 0 \quad 0 \quad \cdots \quad n_1}_{k-i \text{ columns}} & & & & \end{bmatrix}.$$

The next block to the right consists of $k - 2$ columns and is:

$$\begin{bmatrix} 0 & \cdots & 0 & -n_2 & n_2 & 0 & 0 & \cdots & 0 \\ 0 & \cdots & 0 & -n_2 & 0 & n_2 & 0 & \cdots & 0 \\ & \cdots & & \cdots & & & \cdots & & \\ \underbrace{0} & \cdots & \underbrace{0} & -n_2 & \underbrace{0} & \underbrace{0} & & \cdots & n_2 \\ i-3 \text{ columns} & & & & & k-i \text{ columns} & & & \end{bmatrix}.$$

The pattern is now clear.

The first block to the right of the i-th diagonal block consists of the next $(k - [i + 1])$ columns and is

$$\begin{bmatrix} -n_{i+2} & -n_{i+3} & \cdots & -n_k \\ n_{i+1} & 0 & \cdots & 0 \\ 0 & n_{i+1} & \cdots & 0 \\ \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & \cdots & n_{i+1} \end{bmatrix}.$$

The block to the right of this is

$$\begin{bmatrix} 0 & 0 & \cdots & 0 \\ -n_{i+3} & -n_{i+4} & \cdots & -n_k \\ n_{i+2} & 0 & \cdots & 0 \\ 0 & n_{i+2} & \cdots & 0 \\ \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & \cdots & n_{i+2} \end{bmatrix}.$$

Again, the pattern is clear.

At the next step in evaluating the determinant, from column 1 subtract columns $([k-1]+1)$ through $([k-1]+[k-2])$. To column 2, add column $([k - 1] + 1)$ and subtract columns $([k - 1] + [k - 2] + 1)$ through $([k - 1] + [k - 2] + [k - 3])$. In general, to column i, $i = 1, \cdots, k - 1$, add the $i - 1$ columns described as those containing the first column of the diagonal blocks previously set out, and subtract the sum of the next $(k - [i + 1])$ columns, that is, the columns including the $(i + 1)$-st diagonal block.

The result of the above operations is that the first diagonal block has $\sum n_i + 1$ as common diagonal element and zeros elsewhere. The other blocks containing the first $k - 1$ columns are of the form previously described but with $-n_1$ and n_1 replaced by $-(\sum n_i + 1)$ and $\sum n_i + 1$ respectively.

At the next and final step, leave rows $1, \cdots, k - 1$ unaltered.

Consider the next $k - 2$ rows which we now call the first set, the next $k - 3$ rows called the second set, and so on, the i-th set consisting of $(k - [i + 1])$ rows, beginning with row $\sum_{\alpha=1}^{i} (k - \alpha) + 1$. To the j-the row of the i-th set, add row i and subtract row $i + j$, these rows coming from the first $k - 1$ rows of the determinant.

The result of these operations is a determinant with $\sum n_i + 1$ in the first $k - 1$ principal diagonal positions, ones elsewhere in the principal diagonal, and zeros below the principal diagonal. Hence the determinant is as given.

That the inverse elements are correctly given may be checked by multiplying the matrix by the given inverse.

For the treatments versus control procedure, let X_i, $i = 0, 1, \cdots, k$ be random variables measuring some characteristic of a control and k treatments with n_i observations in the i-th sample.

Computation of the test criterion requires us to:

1. Rank jointly the X_0's and X_i's, i fixed, giving rank 1 to the least observation.
2. Add ranks for the variable with fewer observations, here assumed to be the check, to give T_i.
3. Compute the conjugate, T_i'.

Consider $(T_1, \cdots, T_k)$. Again, a recursion formula for finding the number of permutations which give rise to a specific value of $(T_1, \cdots, T_k)$ is given in [13].

The distribution of $(T_1, \cdots, T_k)$ has been shown to have the following parameters [13]:

$$E(T_i) = \mu_i = n_0(n_0 + n_i + 1)/2,$$

$$E(T_i - \mu_i)^2 = \sigma_i^2 = n_0 n_i(n_0 + n_i + 1)/12,$$

$$E(T_i - \mu_i)(T_j - \mu_j) = \sigma_{ij} = n_0 n_i n_j/12,$$

$$\rho_{ij}^2 = n_i n_j/(n_0 + n_i + 1)(n_0 + n_j + 1).$$

It may also be shown that the determinant of the variance-covariance matrix is

$$\prod_0^k n_i(n_0[n_0 + 1])^{k-1}\Big(\sum_0^k n_i + 1\Big)/12.$$

The diagonal and off-diagonal elements of the inverse are, respectively,

$$12\Big(\sum_{\alpha \neq i} n_\alpha + 1\Big)\Big/\Big[n_0(n_0 + 1)n_i\Big(\sum_0^k n_\alpha + 1\Big)\Big],$$

and

$$-12\Big/\Big[n_0(n_0 + 1)\Big(\sum_0^k n_i + 1\Big)\Big].$$

To evaluate the determinant of the variance-covariance matrix, factor $n_0 n_i/12$ from the i-th row of the determinant.
This gives:

$$\frac{n_0^{k-1}\prod_0^k n_i}{12^k}\begin{vmatrix} n_0+n_1+1 & n_2 & \cdots & n_k \\ n_1 & n_0+n_2+1 & \cdots & n_k \\ \cdots & \cdots & \cdots & \cdots \\ n_1 & n_2 & \cdots & n_0+n_k+1 \end{vmatrix}.$$

Next, subtract the k-th row from the i-th row, $i = 1, \cdots, k-1$. We obtain

$$\frac{n_0^{k-1}\prod_0^k n_i}{12^k}\begin{vmatrix} n_0+1 & 0 & \cdots & -(n_0+1) \\ 0 & n_0+1 & \cdots & -(n_0+1) \\ \cdots & \cdots & \cdots & \cdots \\ n_1 & n_2 & \cdots & n_0+n_k+1 \end{vmatrix}.$$

Finally, obtain a new k-th column as the sum of all columns. It is then apparent that the given determinant is correct.

That the given inverse elements are correct is seen by multiplying the matrix by the stated inverse.

From the above information, it is possible to tabulate probabilities for the parent distribution and derived distributions of interest.

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THE ESTIMATION OF REPEATABILITY AND HERITABILITY FROM RECORDS SUBJECT TO CULLING

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1. INTRODUCTION

In any animal breeding selection programme, estimates of repeatability and heritability are needed to choose between the various selection schemes available and also to ensure that the highest possible genetic gains are obtained from the chosen scheme. Estimates of repeatability and heritability are generally subject to large sampling errors. Therefore, the most efficient methods of estimation should be used even if they do involve rather lengthy computations. In this paper, the maximum likelihood estimation of repeatability and heritability from records subject to culling will be considered. The more usual regression estimators are often very inefficient compared with these maximum likelihood estimators.

Suppose that we wish to estimate the repeatability of lactation yield in a herd of dairy cattle. We shall assume that only first and second lactation yields are available and that, if there had been no culling (*i.e.*, if all the cows had had second records as well as first records), the first and second records would have been normally distributed over the herd with means μ_1 and μ_2 , variances σ_1^2 and σ_2^2 and covariance between the two records of the same cow σ_{12} . The first and second records of cow i will be written y_{i1} and y_{i2} respectively. The assumption of normality for the distributions will probably be a reasonably good approximation unless the herd can be split into groups so that any two cows in the same group are much more alike than two cows in different groups. These groups may, for example, be groups of daughters of the same sire or groups of cows according to the year in which they gave their first record or the month in which they calved. Methods are available for making allowances for such groupings, but they will be assumed absent in the rest of this paper. Very rarely will the culling

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in the herd be sufficiently intense or sufficiently highly correlated with future milk yielding capacity to affect seriously the normality of the distributions.

Repeatability is defined as the correlation between two different records of the same cow and is therefore

$$\rho = \sigma_{12}/\sigma_1\sigma_2 .$$

Since we are considering only first and second records, the question of whether the repeatability is the same for all pairs of records will not be discussed. The assumption is frequently made that $\sigma_1^2 = \sigma_2^2$ and, therefore, that repeatability is the same quantity as the regression coefficient of second records on first, $\beta_{21} = \sigma_{12}/\sigma_1^2$. The assumption is made, for example, in the formula given by Lush [1945] for comparing cows with a differing number of records and in the formula given by Lerner [1958] for the ratio of the heritability of the mean of n records to the heritability of a single record. It was also used by Henderson, Kempthorne, Searle and von Krosigk [1959] in their discussion of the disentanglement of environmental and genetic trends from records subject to culling. When $\sigma_1^2 \neq \sigma_2^2$, an estimate of β_{21} is needed for prediction purposes but for other purposes estimates of σ_1^2 and σ_2^2 may also be required. We shall assume in this paper that $\sigma_1^2 = \sigma_2^2 = \sigma^2$, say, and therefore that $\beta_{21} = \rho$. A logarithmic transformation applied to the data may sometimes be useful in satisfying this assumption.

ρ is generally estimated by b, the sample regression coefficient of second records on first. There are two reasons for this. First, b is very simple to calculate and, second, it is an unbiassed estimator of ρ despite any culling that may have been based on the first records. However, when $\sigma_1^2 = \sigma_2^2$ and the first records of all cows are available, whether or not they have second records, b is not the maximum likelihood estimator of ρ. The variance of the second records about their regression on the first estimates $\sigma^2(1 - \rho^2)$ and the variance of all the first records estimates σ^2. These two estimators can be combined to give an estimator of ρ^2. Maximum likelihood makes use of this information as well as the information given by b.

We shall derive the maximum likelihood estimators of ρ and σ^2. We shall show that the efficiency of b as an estimator of ρ, relative to the maximum likelihood estimator, is fairly low for values of the various parameters that may well occur in practice. The bias of the maximum likelihood estimator is shown to be small. This suggests that the maximum likelihood estimator may be worth calculating. The computations involve only the solution of a cubic equation. A section is devoted to an approximate check of the assumption that $\sigma_1^2 = \sigma_2^2$.

Attention has been confined so far to the estimation of repeatability. The methods to be discussed could also be applied to the estimation of heritability from parent-offspring records. The assumption $\sigma_1^2 = \sigma_2^2$ means that, had there been no selection of parents, the variance of the parents and of the offspring would have been equal. In heritability studies, the maximum likelihood method makes use of information about animals that are not parents of animals which also have records. In milk yield studies, this would include information on dams that have only male calves.

2. THE MAXIMUM LIKELIHOOD ESTIMATION OF REPEATABILITY

All the cows have first lactation records but they do not all have second lactation records. We shall assume that the probability that a cow has a second record depends on its first record but not on any other character correlated with the second record. This rules out culling based on information about relatives or on characters such as percentage butter-fat. However, the effect of such culling on the estimates will often be very small and could probably be safely ignored.

Let N cows have a first record and $n \leq N$ cows have a second record. Numbering the cows with a second record $i = 1, 2, \cdots, n$ and the cows without a second record $i = n + 1, n + 2, \cdots, N$, the first records can be written

$$y_{i1} \qquad (i = 1, 2, \cdots, N)$$

and the second records

$$y_{i2} \qquad (i = 1, 2, \cdots, n).$$

The N first records are normally distributed with mean μ_1 and variance σ^2. Because the culling is based only on first records, the distribution of a second record y_{i2}, given the first y_{i1}, is independent of the distribution of the first record and is normal with mean $\mu_2 + \rho(y_{i1} - \mu_1)$ and variance $\sigma^2(1 - \rho^2)$. The likelihood of all the records is therefore

$$L = \frac{1}{(2\pi\sigma^2)^{N/2}} \exp\left\{-\frac{\sum_{i=1}^{N}(y_{i1} - \mu_1)^2}{2\sigma^2}\right\}$$

$$\times \frac{1}{[2\pi\sigma^2(1 - \rho^2)]^{n/2}} \exp\left\{-\frac{\sum_{i=1}^{n}[y_{i2} - \mu_2 - \rho(y_{i1} - \mu_1)]^2}{2\sigma^2(1 - \rho^2)}\right\}$$

and the log likelihood is, apart from a constant,

$$\ln L = -\frac{(n+N)}{2}\ln\sigma^2 - \frac{n}{2}\ln(1-\rho^2) - \frac{(1-\rho^2)\sum_{i=1}^{N}(y_{i1}-\mu_1)^2 + \sum_{i=1}^{n}[y_{i2}-\mu_2-\rho(y_{i1}-\mu_1)]^2}{2\sigma^2(1-\rho^2)}. \quad (2.1)$$

Kempthorne and von Krosigk (Henderson, Kempthorne, Searle and von Krosigk [1959]) suggested the use of maximum likelihood to estimate repeatability from records subject to culling. They derived the log likelihood when the cows were classified into groups and when the number of records for each cow was perfectly general. They derived very lengthy equations from which the maximum likelihood estimates of the parameters could be determined. In this paper, we are studying in greater detail the special case when there is no grouping of the cows and when there are at most only two records per cow.

(2.1) can be written

$$\ln L = -\frac{(n+N)}{2}\ln\sigma^2 - \frac{n}{2}\ln(1-\rho^2) - \frac{Ns^2}{2\sigma^2} - \frac{n(\rho^2\Sigma_1^2+\Sigma_2^2-2\rho\Sigma_{12})}{2\sigma^2(1-\rho^2)} - \frac{N(\bar{y}-\mu_1)^2}{2\sigma^2} - \frac{n[\bar{y}_2-\mu_2-\rho(\bar{y}_1-\mu_1)]^2}{2\sigma^2(1-\rho^2)} \quad (2.2)$$

where

$$s^2 = \frac{\sum_{i=1}^{N}(y_{i1}-\bar{y})^2}{N}, \qquad \Sigma_1^2 = \frac{\sum_{i=1}^{n}(y_{i1}-\bar{y}_1)^2}{n},$$

$$\Sigma_2^2 = \frac{\sum_{i=1}^{n}(y_{i2}-\bar{y}_2)^2}{n}, \qquad \Sigma_{12} = \frac{\sum_{i=1}^{n}(y_{i1}-\bar{y}_1)(y_{i2}-\bar{y}_2)}{n},$$

$$\bar{y} = \frac{\sum_{i=1}^{N}y_{i1}}{N}, \qquad \bar{y}_1 = \frac{\sum_{i=1}^{n}y_{i1}}{n} \quad \text{and} \quad \bar{y}_2 = \frac{\sum_{i=1}^{n}y_{i2}}{n}.$$

The maximum likelihood estimators of μ_1 and μ_2 are clearly given by

$$\hat{\mu}_1 = \bar{y} \quad \text{and} \quad \hat{\mu}_2 = \bar{y}_2 - \hat{\beta}(\bar{y}_1 - \mu_1).$$

Also

$$\frac{\partial(\ln L)}{\partial(\sigma^2)} = -\frac{(n+N)}{2\sigma^2} + \frac{Ns^2}{2\sigma^4} + \frac{n(\rho^2\Sigma_1^2+\Sigma_2^2-2\rho\Sigma_{12})}{2\sigma^4(1-\rho^2)} + \frac{N(\bar{y}-\mu_1)^2}{2\sigma^4} + \frac{n[\bar{y}_2-\mu_2-\rho(\bar{y}_1-\mu_1)]^2}{2\sigma^4(1-\rho^2)} \quad (2.3)$$

and

$$\frac{\partial(\ln L)}{\partial\rho} = \frac{n\rho}{1-\rho^2} - \frac{n[\rho(\Sigma_1^2+\Sigma_2^2) - (1+\rho^2)\Sigma_{12}]}{\sigma^2(1-\rho^2)^2} + \frac{n(\bar{y}_1-\mu_1)[\bar{y}_2-\mu_2-\rho(\bar{y}_1-\mu_1)]}{\sigma^2(1-\rho^2)} - \frac{n\rho[\bar{y}_2-\mu_2-\rho(\bar{y}_1-\mu_1)]^2}{\sigma^2(1-\rho^2)^2}. \tag{2.4}$$

By setting (2.3) and (2.4) equal to zero and substituting the maximum likelihood estimators of μ_1 and μ_2, $\hat{\rho}$ satisfies the cubic

$$(Ns^2 - n\Sigma_1^2)\hat{\rho}^3 - (N-n)\Sigma_{12}\hat{\rho}^2 + [(n+N)\Sigma_1^2 - N(s^2-\Sigma_2^2)]\hat{\rho} - (n+N)\Sigma_{12} = 0. \tag{2.5}$$

This equation will have one and only one root between -1 and $+1$ of the same sign as the simple estimator $b = \Sigma_{12}/\Sigma_1^2$. There may be two other roots between -1 and $+1$ of opposite sign to b. The formula for $\hat{\sigma}^2$ is

$$\hat{\sigma}^2 = \frac{\hat{\rho}(\Sigma_1^2+\Sigma_2^2) - (1+\hat{\rho}^2)\Sigma_{12}}{\hat{\rho}(1-\hat{\rho}^2)}. \tag{2.6}$$

When there is no culling, $s^2 = \Sigma_1^2$ and

$$\hat{\rho} = \frac{2\Sigma_{12}}{\Sigma_1^2+\Sigma_2^2}.$$

When $\sigma_1^2 = \sigma_2^2$, the maximum likelihood estimator of the correlation coefficient has the arithmetic rather than the geometric mean of the two sample variances in the denominator.

To obtain the asymptotic variance of $\hat{\rho}$, we need the expected values of the second-order partial derivatives of ln L with respect to μ_1, μ_2, ρ and σ^2. These can be derived from a knowledge of the expected values of s^2, Σ_2^2 and Σ_{12}. Σ_1^2 depends on the method of culling and so will be taken as fixed. For reasons to be given later, we shall calculate the expected values when $\sigma_1^2 \neq \sigma_2^2$. Clearly, $E(s^2) = (N - 1/N)\sigma_1^2$. By writing

$$y_{i2} = \mu_2 + \frac{\rho\sigma_2}{\sigma_1}(y_{i1}-\mu_1) + \sigma_2\sqrt{1-\rho^2}\,e_{i2.1},$$

so that $e_{i2.1}$ has a standard normal distribution independent of y_{i1},

$$\Sigma_2^2 = \frac{1}{n}\sum_{i=1}^{n}\left[\frac{\rho\sigma_2}{\sigma_1}(y_{i1}-\bar{y}_1) + \sigma_2\sqrt{1-\rho^2}\,(e_{i2.1}-\bar{e}_{.2.1})\right]^2,$$

and, therefore, for given Σ_1^2,

$$E(\Sigma_2^2) = \frac{\rho^2\sigma_2^2}{\sigma_1^2}\Sigma_1^2 + \frac{(n-1)}{n}\sigma_2^2(1-\rho^2).$$

Similarly,

$$E(\Sigma_{12}) = \frac{\rho\sigma_2}{\sigma_1}\Sigma_1^2 .$$

Also, with $\sigma_1^2 = \sigma_2^2$, $E(\bar{y} - \mu_1)^2 = \sigma^2/N$, $E[\bar{y}_2 - \mu_2 - \rho(\bar{y}_1 - \mu_1)]^2 = \sigma^2(1-\rho^2)/n$ and $E\{(\bar{y}_1 - \mu_1)[\bar{y}_2 - \mu_2 - \rho(\bar{y}_1 - \mu_1)]\} = 0$. After considerable algebra the asymptotic variance—covariance matrix for $\hat{\mu}_1$, $\hat{\mu}_2$, $\hat{\sigma}^2$ and $\hat{\rho}$ is found to be V, where

$$\mathbf{V}^{-1} = \begin{bmatrix} \frac{N}{\sigma^2} + \frac{n\rho^2}{\sigma^2(1-\rho^2)} & -\frac{n\rho}{\sigma^2(1-\rho^2)} & 0 & -\frac{n\rho(\bar{y}_1-\mu_1)}{\sigma^2(1-\rho^2)} \\ -\frac{n\rho}{\sigma^2(1-\rho^2)} & \frac{n}{\sigma^2(1-\rho^2)} & 0 & \frac{n(\bar{y}_1-\mu_1)}{\sigma^2(1-\rho^2)} \\ 0 & 0 & \frac{n+N}{2\sigma^4} & -\frac{n\rho}{\sigma^2(1-\rho^2)} \\ -\frac{n\rho(\bar{y}_1-\mu_1)}{\sigma^2(1-\rho^2)} & \frac{n(\bar{y}_1-\mu_1)}{\sigma^2(1-\rho^2)} & -\frac{n\rho}{\sigma^2(1-\rho^2)} & \theta \end{bmatrix}$$

and

$$\theta = \frac{n}{\sigma^2(1-\rho^2)^2}[(1-\rho^2)\Sigma_1^2 + 2\rho^2\sigma^2] + \frac{n(\bar{y}_1-\mu_1)^2}{\sigma^2(1-\rho^2)}.$$

The asymptotic variance of $\hat{\rho}$ is

$$V(\hat{\rho}) = \frac{(N+n)(1-\rho^2)^2}{n[(N+n)(1-\rho^2)\Sigma_1^2/\sigma^2 + 2N\rho^2]}.$$

Writing $n/N = S$, so that $(1 - S)$ is the culling intensity, and $\Sigma_1^2/\sigma^2 = 1/c$, where c measures the effect of the culling on the variance of the first records and is therefore a possible measure of the efficiency of the culling,

$$V(\hat{\rho}) = \frac{1}{n}\frac{(1+S)(1-\rho^2)^2}{\left[\frac{(1+S)(1-\rho^2)}{c} + 2\rho^2\right]}. \tag{2.7}$$

We shall now derive the approximate bias in $\hat{\rho}$ as an estimator of ρ. By substituting $\hat{\rho} = \rho + \delta$ in (2.5) and ignoring terms in δ^3 and δ^4,

$$\delta \doteq -\frac{(Ns^2 - n\Sigma_1^2)\rho^3 - (N-n)\Sigma_{12}\rho^2 + [(n+N)\Sigma_1^2 - N(s^2 - \Sigma_2^2)]\rho - (n+N)\Sigma_{12}}{3(Ns^2 - n\Sigma_1^2)\rho^2 - 2(N-n)\Sigma_{12}\rho + [(n+N)\Sigma_1^2 - N(s^2 - \Sigma_2^2)]}. \tag{2.8}$$

Approximating $E(\delta)$ by taking expected values separately in the numerator and denominator,

$$E(\delta) \doteq -\frac{\rho(1-\rho^2)\sigma^2(n-N)}{\Sigma_i^2 n(n+N)(1-\rho^2)+\sigma^2[(n-N)+\rho^2(2nN+N-3n)]}.$$

To order $1/n$,

$$E(\delta) = \frac{\rho(1-\rho^2)(1-S)}{n\left[\frac{(1+S)(1-\rho^2)}{c}+2\rho^2\right]}. \tag{2.9}$$

Therefore, from (2.7), the approximate ratio of the bias to the standard deviation is

$$\frac{E(\delta)}{\sqrt{V(\hat{\beta})}} \doteq \frac{\rho(1-S)}{\sqrt{n}\sqrt{1+S}\left\{\frac{1+S}{c}(1-\rho^2)+2\rho^2\right\}^{1/2}}$$

$$\leq \frac{\rho(1-S)}{\sqrt{n}\sqrt{1+S}}\,\mathrm{Max}\left[\sqrt{\frac{c}{1+S}},\,1/\sqrt{2}\right].$$

If n is reasonably large, the bias in $\hat{\beta}$ is unlikely to be serious. The bias will become relatively more important when estimates of ρ from different sources are pooled.

3. ESTIMATION OF σ_1^2 AND σ_2^2 WHEN $\sigma_1^2 \neq \sigma_2^2$

In the previous section we derived the expected values of s^2, Σ_2^2 and Σ_{12} for given Σ_1^2 when $\sigma_1^2 \neq \sigma_2^2$. They were

$$E(s^2) = \frac{N-1}{N}\sigma_1^2,$$

$$E(\Sigma_2^2) = \frac{\rho^2\sigma_2^2}{\sigma_1^2}\Sigma_1^2 + \frac{(n-1)}{n}\sigma_2^2(1-\rho^2),$$

and

$$E(\Sigma_{12}) = \frac{\rho\sigma_2}{\sigma_1}\Sigma_1^2.$$

Apart from the usual slight differences in the multipliers, important only for small n and N, the following estimators of σ_1^2, $\beta = \rho\sigma_2/\sigma_1$ and $\sigma_2^2(1-\rho^2)$ are the maximum likelihood estimators when $\sigma_1^2 \neq \sigma_2^2$,

$$\hat{\sigma}_1^2 = Ns^2/(N-1),$$

$$\hat{\beta}_{21} = b = \Sigma_{12}/\Sigma_1^2,$$

and

$$\widehat{\sigma_2^2(1-\rho^2)} = \frac{n}{n-2}[\Sigma_2^2 - \Sigma_{12}^2/\Sigma_1^2].$$

From the expected values of s^2, Σ_2^2 and Σ_{12} given in the previous section these estimators are all unbiassed. The maximum likelihood estimator of σ_2^2/σ_1^2 is

$$\widehat{\left(\frac{\sigma_2^2}{\sigma_1^2}\right)} = \frac{\Sigma_{12}^2}{\Sigma_1^4} + \frac{\Sigma_2^2 - \Sigma_{12}^2/\Sigma_1^2}{s^2}. \tag{3.1}$$

No exact method is available for constructing a confidence interval for σ_2^2/σ_1^2 except when $n = N$, *i.e.*, when there is no culling (see Curnow [1957] for references and for a method to be used when the data are grouped). The asymptotic variance of $\widehat{(\sigma_2^2/\sigma_1^2)}$ could be derived and used to provide an approximate confidence interval. This would give some indication of the importance of the assumption that $\sigma_1^2 = \sigma_2^2$. A simpler, but much less sensitive, test of whether $\sigma_2^2 > \sigma_1^2$ could be based on the fact that the quantity

$$\frac{(N-1)n\sigma_1^2}{N(n-2)\sigma_2^2(1-\rho^2)} \times \frac{\Sigma_2^2 - \Sigma_{12}^2/\Sigma_1^2}{s^2},$$

which compares a χ^2-value from the variation of the second records about their regression on the first with a χ^2-value from the variation of all the first records, has an F-distribution with $n-2$ and $N-1$ degrees of freedom.

$$F = \frac{(N-1)n}{N(n-2)} \frac{\Sigma_2^2 - \Sigma_{12}^2/\Sigma_1^2}{s^2}$$

significantly greater than $F = 1$ would suggest that $\sigma_2^2(1-\rho^2) > \sigma_1^2$ and, therefore, that $\sigma_2^2 > \sigma_1^2$.

4. THE EFFICIENCY OF THE SIMPLE REGRESSION ESTIMATOR OF REPEATABILITY

The statistic $b = \Sigma_{12}/\Sigma_1^2$ is very easy to calculate and is the one generally used to estimate repeatability. It is the only possible estimator if first records are available only for those cows also having second records. Providing that culling is based solely on the first lactation yields, b is always an unbiassed estimator of $\beta_{21} = \rho\sigma_2/\sigma_1$, but an unbiassed estimator of ρ only when $\sigma_1^2 = \sigma_2^2$. In this paper we are assuming $\sigma_1^2 = \sigma_2^2$. The variance of b is

$$V(b) = \sigma^2/n\Sigma_1^2 = c/n. \tag{4.1}$$

From (2.7), the asymptotic efficiency of b relative to the maximum likelihood estimator, $\hat{\rho}$, is therefore

$$Eff. = \frac{(1 + S)(1 - \rho^2)^2}{(1 + S)(1 - \rho^2) + 2c\rho^2}.$$

The values of this efficiency are shown in Table 1 for various values of S, ρ and c.

The following considerations suggest that c is unlikely to be greater than $c = 2$. Let the N cows be reduced to LN by accidental factors uncorrelated with the level of yield. Then a proportion $P = n/LN = S/L$ can be selected on the basis of first lactation yield. Assume that the selection is of the proportion S/L of the herd having the highest yields and that n and LN are sufficiently large that the effect of the selection

TABLE 1

THE ASYMPTOTIC EFFICIENCY OF THE SIMPLE REGRESSION ESTIMATOR OF REPEATABILITY RELATIVE TO THE MAXIMUM LIKELIHOOD ESTIMATOR

Overall Selection Intensity ($S = n/N$)	Repeatability (ρ)	$c = \sigma^2/\Sigma_1^2$				
		1/2	1	4/3	2	4
1/4	0	1.00	1.00	1.00	1.00	1.00
	1/4	0.95	0.90	0.88	0.82	0.70
	1/2	0.79	0.65	0.58	0.48	0.32
	3/4	0.49	0.33	0.27	0.20	0.11
	1	0	0	0	0	0
1/2	0	1.00	1.00	1.00	1.00	1.00
	1/4	0.96	0.92	0.89	0.85	0.74
	1/2	0.82	0.69	0.63	0.53	0.36
	3/4	0.54	0.37	0.30	0.23	0.13
	1	0	0	0	0	0
3/4	0	1.00	1.00	1.00	1.00	1.00
	1/4	0.96	0.93	0.91	0.87	0.77
	1/2	0.84	0.72	0.66	0.57	0.40
	3/4	0.58	0.40	0.34	0.25	0.15
	1	0	0	0	0	0
1	0	1.00	1.00	1.00	1.00	1.00
	1/4	0.97	0.94	0.92	0.88	0.79
	1/2	0.86	0.75	0.69	0.60	0.43
	3/4	0.61	0.44	0.37	0.28	0.16
	1	0	0	0	0	0

can be approximated by the truncation of the top P proportion of an infinite normal population with mean μ_1 and variance σ^2. The variance of the selected first records will then be

$$\Sigma_1^2 = \sigma^2[1 - \nu(\nu - T)],$$

where $\nu = Z/P$ and Z and T are the ordinate and abscissa at the point above which lies a proportion P of the population (Finney [1957] derives this formula and provides a table of values of $\nu' = \nu(\nu - T)$ for various values of P). The division of the overall selection intensity, S, between L and P is never complete and is certainly never known exactly. However, P is generally considerably larger than S, *i.e.*, there is a large amount of random culling and not so much actual selection. The value of c is

$$c = \frac{\sigma^2}{\Sigma_1^2} = 1/[1 - \nu(\nu - T)].$$

For various P, it takes the following values:

$$P = 0.95 \quad 0.9 \quad 0.8 \quad 0.7 \quad 0.6 \quad 0.5 \quad 0.1,$$

$$c = 1.24 \quad 1.40 \quad 1.72 \quad 2.03 \quad 2.37 \quad 2.75 \quad 5.91.$$

In practice, P is unlikely to be less than $P = 0.7$ and therefore c is unlikely to exceed $c = 2$. Table 1 does include $c = 4$ to illustrate the effect of intense selection based on yield and $c = \frac{1}{2}$ to illustrate the effect of a selection scheme that results in an increased rather than a decreased variance. The efficiency is the same for ρ as for $-\rho$ and so ρ is shown as positive in the table. In practice, ρ is very unlikely to be negative.

When $\rho = 0$, the efficiency of the simple regression estimator is 1. When $\rho = 1$, it is 0. For intermediate values of ρ, the efficiency increases rather slowly with S for fixed c, but decreases fairly rapidly with increasing c. For all values of c and S, the efficiency is very low for high values of ρ. As an example of the efficiency likely to occur in the estimation of the repeatability of lactation records, the efficiency is 0.66 when $c = \frac{4}{3}$, $\rho = \frac{1}{2}$ and $S = \frac{3}{4}$. In this case, the maximum likelihood estimator would certainly be worth calculating.

5. THE ESTIMATION OF REPEATABILITY BY AN ANALYSIS OF VARIANCE

Sometimes the effect of culling based on the first records is ignored and ρ estimated from a least squares analysis of variance of the $N + n$ first and second records. Table 2 shows this analysis of variance. The "cows and periods" sum of squares has been split into both "cows

adjusting for periods and periods ignoring cows" and "cows ignoring periods and periods adjusting for cows". By a period difference is meant an average difference between first and second lactation records. The expected values of four important mean squares are shown. Δ_1, Δ_2 and Δ_3 are defined at the foot of the table and vanish only if the culling is random with respect to the first records. Two cases need to be distinguished. In the first we assume $\mu_1 = \mu_2$ and in the second we do not. We shall use the reference numbers at the right of the table. If $\mu_1 = \mu_2$, mean square 2 and a mean square obtained by pooling sums of squares 3 and 4 are used to estimate σ^2 and ρ. This is exactly equivalent to an analysis of a one way classification with unequal sub-class numbers (Snedecor, [1956], §10.16). If $\mu_1 \neq \mu_2$, mean squares 1 and 4 are used to estimate σ^2 and ρ. There seems to be little justification for using mean square 2 with mean square 4. One or other is biassed or inefficient according as $\mu_1 \neq \mu_2$ or $\mu_1 = \mu_2$.

The bias in any of the above methods is difficult to determine without some knowledge of the effect of culling on the expected values of $\sum_1^2 - [(n-1)/n]\sigma^2$, $\bar{y}_1 - \mu_1$, $(\bar{y}_1 - \mu_1)^2 - \sigma^2/n$ and $(\bar{y}_1 - \mu_1)\bar{y} - \sigma^2/N$. However, these unknown biasses are clearly undesirable. Since the method of estimation described in this paper is the maximum likelihood method whether or not the culling is random with respect to first records, it is to be preferred. If culling is random with respect to first records, c can be substituted as $c = 1$ in the formulae for the asymptotic bias and variance of the maximum likelihood estimator and the asymptotic efficiency of the regression method.

Wadell [1961] has given a method for estimating ρ when the culling is equivalent to truncation of the first lactation yields. His estimate of ρ is a function of $\bar{y}_1$, $\bar{y}_2$, s^2, Σ_1^2 and the mean squares 2, 3, and 4 of Table 2. The estimate has a negligible bias for large values of n but its variance is not given and therefore its efficiency is unknown.

6. A NUMERICAL EXAMPLE

Dr. A. E. Freeman of the Department of Animal Husbandry, Iowa State University has kindly made available to me some Complete Herd Improvement Registry Records of an Iowa Board of Control herd of Holstein-Friesian cattle. The records included some first and second lactation yields made in various years but expressed as deviations from the herd average for each particular year. The cows were milked twice daily and their yields expressed as mature equivalent 305-day lactation yields.

The values of the various relevant statistics for a sample of the records were:

TABLE 2

ANALYSIS OF VARIANCE OF FIRST AND SECOND RECORDS

Source	d.f	Sums of Squares	Expected Values of Mean Squares	Ref. Nos.
Cows adj. Periods	$N-1$	$\frac{n}{2}(\Sigma_2^2+2\Sigma_{12}-\Sigma_1^2)+Ns^2$	$\sigma^2(1-\rho)+\frac{n+N-2}{N-1}\rho\sigma^2$ $+\frac{n}{2(N-1)}(\rho^2+2\rho-1)\Delta_1$	1
Periods ign. Cows	1	$\frac{nN}{N+n}(\bar{y}-\bar{y}_2)^2$		
Cows and Periods	N	$\frac{n}{2}(\Sigma_2^2+2\Sigma_{12}-\Sigma_1^2)+Ns^2$ $+\frac{nN}{N+n}(\bar{y}-\bar{y}_2)^2$		
Cows ign. Periods	$N-1$	$\frac{n}{2}(\Sigma_2^2+2\Sigma_{12}-\Sigma_1^2)+Ns^2$ $+\frac{nN}{N+n}(\bar{y}-\bar{y}_2)^2-\frac{n}{2}(\bar{y}_1-\bar{y}_2)^2$	$\sigma^2(1-\rho)$ $+\frac{(n+N)^2-(N+3n)}{(N-1)(N+n)}\rho\sigma^2$ $+\frac{n(N-n)}{2(N-1)(N+n)}(\mu_2-\mu_1)^2$ $+\frac{n}{N-1}\Delta_2$	2
Periods adj. Cows	1	$\frac{n}{2}(\bar{y}_1-\bar{y}_2)^2$	$\sigma^2(1-\rho)+\frac{n}{2}(\mu_2-\mu_1)^2+n(1-\rho)\Delta_3$	3
Error	$n-1$	$\frac{n}{2}(\Sigma_2^2-2\Sigma_{12}+\Sigma_1^2)$	$\dot{\sigma}^2(1-\rho)+\frac{n(1-\rho)^2}{2(n-1)}\Delta_1$	4
TOTAL	$N+n-1$	$n\Sigma_2^2+Ns^2+\frac{Nn}{N+n}(\bar{y}-\bar{y}_2)^2$		
Adj. for mean	1	$\frac{(N\bar{y}+n\bar{y}_2)^2}{N+n}$		

$\Delta_1 = \Sigma_1^2 - \frac{n-1}{n}\sigma^2,$

$\Delta_2 = \frac{1}{2}(\rho^2+2\rho-1)\Delta_1 + \frac{1}{2}\left(\frac{N-n}{N+n}\rho^2+2\rho-1\right)(D^2-\sigma^2/n)$

$+\left(\frac{N-n}{N+n}\rho\mu_2+\mu_2-\mu_1+\rho\mu_1\right)D-\frac{2N\rho}{N+n}(D\bar{y}-\sigma^2/N),$

$\Delta_3 = \frac{1}{2}(1-\rho)(D^2-\sigma^2/n)-(\mu_2-\mu_1)D$ and $D=\bar{y}_1-\bar{y}_1$.

$N = 220, \quad n = 150, \quad S = 0.682;$

$\bar{y} = -1.118, \quad \bar{y}_1 = 1.147, \quad \bar{y}_2 = -0.207;$

$s^2 = 286.55, \quad \Sigma_1^2 = 270.51, \quad \Sigma_{12} = 125.85$ and $\Sigma_2^2 = 354.98.$

The maximum likelihood estimator of σ_2^2/σ_1^2 (3.1) is $\widehat{(\sigma_2^2/\sigma_1^2)} = 1.25$. This value is almost certainly not significantly greater than $\sigma_2^2/\sigma_1^2 = 1$. However, it is sufficiently large to raise some doubts about the assumption that $\sigma_2^2 = \sigma_1^2$. The estimate of $\sigma_2^2(1-\rho^2)$ is greater, but not

significantly greater, than the estimate of σ_1^2. However, for illustrative purposes we shall assume $\sigma_2^2 = \sigma_1^2$.

Equation (2.5) for $\hat{\rho}$ is

$$\hat{\rho}^3 - 0.3922\hat{\rho}^2 + 5.1257\hat{\rho} - 2.0728 = 0.$$

The simple regression estimator of ρ is

$$b = \Sigma_{12}/\Sigma_1^2 = 0.465.$$

Three cycles of an iteration based on formulae (2.8) and with $\hat{\rho}_0 = b$ as the initial solution show that the value of $\hat{\rho}$ is, to three decimal places,

$$\hat{\rho} = 0.404.$$

This is the only real root of the maximum likelihood equation for $\hat{\rho}$. The two estimators together with their estimated standard errors [(2.7) and (4.1)] are therefore:

$$b = 0.465 \pm 0.084$$

and

$$\hat{\rho} = 0.404 \pm 0.069.$$

The latter standard error is an asymptotic standard error. The estimated efficiency of the regression estimator is only 67 percent and so $\hat{\rho}$ is probably well worth calculating. The estimated asymptotic bias (2.9) is very small,

$$\widehat{E(\delta)} = 0.0004.$$

The maximum likelihood estimator of σ^2 (2.6) is $\hat{\sigma}^2 = 314.46$. This agrees well with the value $s^2 = 286.55$ used above in estimating $E(\delta)$ and the standard errors of b and $\hat{\rho}$.

The estimated value of c is

$$\hat{c} = s^2/\Sigma_1^2 = 1.059.$$

This value of c suggests that there has been very little selection based on first lactation yield in this particular sample of records. The standardized selection differential

$$(\bar{y}_1 - \bar{y})/s = 0.134$$

suggests that the effective selection intensity P was near 0.93.

7. SUMMARY

The maximum likelihood estimation of repeatability from first and second lactation records of a herd subject to culling is discussed. The

method is applicable only when it can be assumed that, had there been no culling, the variances of the first and the second lactation records would have been equal, and when all the first records are available whether or not the cow has a second record. The efficiency of the more usual estimate of repeatability, based on the regression of second records on first records, is shown to be low when the repeatability is high. In many cases the calculation of the maximum likelihood estimate would seem to be well worthwhile. The use of the method in estimating heritability is mentioned. An illustrative example is given.

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THREE CLASSES OF UNIVARIATE DISCRETE DISTRIBUTIONS

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1. INTRODUCTION

Families of descrete distributions have been developed and studied by many authors, including, Neyman [1939], Feller [1943], Skellam [1952], Beall and Rescia [1953] and Gurland [1957, 1958]. These families are of three types:

$$\text{Type } A: \quad g_A(z) = \exp\{h(z)\},$$

$$\text{Type } B: \quad g_B(z) = \{h(z)\}^a,$$

$$\text{Type } C: \quad g_C(z) = c \log\{h(z)\},$$

where $g(z)$ represents a probability generating function (p.g.f.) and $h(z)$ is a p.g.f., except possibly for additive and multiplicative constants. The aim of this paper is to set up formulae for certain statistics for these types. It is hoped that these will be of use to reseach workers in practical fields, who will be formulating compound and generalised distributions of these types by using specific forms of $h(z)$.

2. RECURRENCE RELATIONS FOR PROBABILITIES

Notations: Let the r-th derivation of $f(z)$ be denoted as $f^{(r)}(z)$. Also let

$$P_r = \{g^{(r)}(z)/r!\}\,|_{z=0}\,, \tag{1}$$

and

$$\pi_r = \{h^{(r)}(z)/r!\}\,|_{z=0}\,. \tag{2}$$

By the definition of $g(z)$, it is clear that P_r denotes the probability of the r-th count in $g(z)$ and π_r, the probability of the r-th count, excepting possibly for additive and multiplicative constants.

Type A: Here

$$g_A(z) = \exp\{h(z)\}.$$

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Successive differentiation leads to

$$g_A^{(r)}(z) = \sum_{k=1}^{r} \binom{r-1}{k-1} h^{(k)}(z) g_A^{(r-k)}(z). \tag{3}$$

Hence, on letting $z = 0$, we have

$$P_r = \sum_{k=1}^{r} k\pi_k P_{r-k}/r \quad \text{with} \quad P_0 = \exp(\pi_0). \tag{4}$$

Type B: Here

$$g_B(z) = \{h(z)\}^n.$$

Successive differentiation of $h(z)g_B^{(1)}(z) = ng_B(z)h^{(1)}(z)$ leads to

$$\sum_{k=1}^{r} \binom{r-1}{k-1} h^{(k-1)}(z) g_B^{(r-k+1)}(z) = n \sum_{k=1}^{r} \binom{r-1}{k-1} h^{(k)}(z) g_B^{(r-k)}(z). \tag{5}$$

Hence, on letting $z = 0$, we have

$$P_r = \sum_{k=1}^{r} (nk - r + k)\pi_k P_{r-k}/r\pi_0 \quad \text{with} \quad P_0 = \pi_0^n. \tag{6}$$

Type C: Here

$$g_C(z) = c \log \{h(z)\} \quad \text{where} \quad c = \log \{h(1)\}^{-1}.$$

Successive differentiation of $h(z)g_C^{(1)}(z) = ch^{(1)}(z)$ leads to

$$h(z)g_C^{(r)}(z) = ch^{(r)}(z) - \sum_{k=1}^{r-1} \binom{r-1}{k} h^{(k)}(z) g_C^{(r-k)}(z). \tag{7}$$

Hence, on letting $z = 0$, we have

$$P_r = \{rc\pi_r - \sum_{k=1}^{r-1} (r-k)\pi_k P_{r-k}\}/r\pi_0 \quad \text{with} \quad P_0 = c \log \pi_0. \tag{8}$$

3. FACTORIAL CUMULANTS

Notations: Let

$$\mu'_{[r]} = \{h^{(r)}(z)\}\,|_{z=1}, \tag{9}$$

$$M'_{[r]} = \{g^{(r)}(z)\}\,|_{z=1}, \tag{10}$$

and

$$K_{[r]} = \{(d/dz)^r \log g(z)\}\,|_{z=1}. \tag{11}$$

From the definition of factorial cumulants, it is clear that $\mu'_{[r]}$ is the r-th factorial moment of $h(z)$ if $h(z)$ is a p.g.f. and $M'_{[r]}$ and $K_{[r]}$ are respectively r-th factorial moment and r-th factorial cumulant of $g(z)$.

Type A: Here $\log \{g_A(z)\} = h(z)$ and hence,

$$K_{(r)} = \mu'_{(r)} . \tag{12}$$

Type B: Here

$$\phi(z) = \log g_B(z) = n \log h(z).$$

Hence, on using (11), it is clear that r-th factorial cumulant of $g_B(z)$ is n times the r-th factorial cumulant of $h(z)$ if $h(z)$ is a p.g.f. Also on using (7) (with necessary modifications), (9) and (11), we have

$$K_{(r)} = n\mu'_{(r)} - \sum_{k=1}^{r-1} \binom{r-1}{k} \mu'_{(k)} K_{(r-k)} . \tag{13}$$

Type C: Here, it is easy to give a recurrence relation for factorial moments $M'_{(r)}$ rather than factorial cumulants. By using (7), (9) and (10), this relation can be shown to be

$$M'_{(r)} = \left\{ c\mu'_{(r)} - \sum_{k=1}^{r-1} \binom{r-1}{k} \mu'_{(k)} M'_{(r-k)} \right\} / \mu'_0 , \tag{14}$$

where $\mu'_0 = h(1)$. The factorial cumulants can be obtained from (14) by using the relations

$$K_{(1)} = M'_{(1)} , \qquad K_{(2)} = M'_{(2)} - M'^2_{(1)} ,$$
$$K_{(3)} = M'_{(3)} - 3M'_{(2)}M'_{(1)} + 2M'^3_1 , \qquad \text{etc.}$$

4. SPECIAL CASES

Notation: If a variate has either a Binomial or a Negative Binomial law as a special case, we say that it has a general binomial law.

Type A: From the form of the Poisson-Binomial, Negative-Binomial, generalised Polya Aeppli, Beall and Rescia [1953] and Neyman's Types A, B, and C, it is clear that they belong to this form. It is to be noted, that, if in the classical problem of egg masses and larvae, the egg masses have a Poisson distribution with p.g.f. $\exp[\lambda(z-1)]$ and the larvae within an egg mass, a distribution with p.g.f. $w(z)$, then the distribution of the larvae over the whole field is $\exp[\lambda\{w(z)-1\}]$ which is of Type A with $h(z) = \lambda\{w(z)-1\}$.

Some important distributions with their recurrence relations are:

(i) Poisson-Hypergeometric distribution [1958]: Here

$$w(z) = \sum_{r=0}^{\infty} \binom{k}{r} \alpha_{(r)} m^r (z-1)^r / (\alpha+\beta)_{(r)} \tag{15}$$

where

$$\alpha_{(r)} = \alpha(\alpha+1)(\alpha+2)\cdots(\alpha+r-1), \qquad \binom{k}{r} = k^{(r)}/r!,$$

$k^{(r)} = k(k-1)\cdots(k-r+1)$, $\alpha_{(0)} = 1$, $k^{(0)} = 1$ and α, β, m and k are such that $w^{(r)}(0)/r! = \pi_r$ is positive. The above distribution was first given by Gurland [1958]. The recurrence relation in probabilities is

$$P_r = \lambda \sum_{s=1}^{r} s\pi_s P_{r-s}/r \tag{16}$$

where $P_0 = \exp\{\lambda(\pi_0 - 1)\}$, and

$$\pi_r = \frac{\alpha + \beta + r - 2 - m(\alpha - k + 2r - 3)}{r(1-m)}\pi_{r-1} - \frac{(\alpha + r - 1)(k - r + 2)m}{r(r-1)(1-m)}\pi_{r-2}, \tag{17}$$

$$\pi_0 = \sum_{s=0}^{\infty} \alpha_{(s)}(-k)_{(s)}m^s/s!(\alpha+\beta)_{(s)} \quad \text{and} \quad \pi_1 = -\frac{d\pi_0}{dm}.$$

For the particular cases of the above distribution, we may refer to Gurland [1958]. The recurrence relation for factorial cumulants is

$$K_{[r]} = \lambda\alpha_{(r)}k^{(r)}m^r/(\alpha+\beta)_{(r)}. \tag{18}$$

(ii) Poisson-Power series distribution:

$$w(z) = \sum_{i=0}^{\infty} a_i z^i, \tag{19}$$

where a_i's are constants such that $w(z)$ is convergent for some z. The recurrence relation for probabilities is

$$P_r = \lambda \sum_{s=1}^{r} s a_s P_{r-s}/r \quad \text{with} \quad P_0 = \exp\{\lambda(a_0 - 1)\}. \tag{20}$$

The above distribution was first given by Maritz [1952].

Type B: Let the distribution of egg masses be a general binomial with p.g.f. $(1 - p + pz)^n$. Then the distribution of the larvae over the whole field is $[1 - p + pw(z)]^n$, i.e. the Type B distribution with $h(z) = \{1 - p + pw(z)\}$. When $n = 1$, this leads to the distribution with p.g.f. $w(z)$ with an addition (or subtraction) of zeros. If $n > 1$ or $n < 0$, this can be regarded as n-th confluent of $w(z)$.

Some important distributions with their recurrence relations are:

(i) G. Binomial-Hypergeometric distribution: Here $w(z)$ is the same as given in (15). This was first stated by Gurland [1958] in the special case when $n < 0$, $p < 0$. The recurrence relation in probabilities is

$$P_r = p \sum_{s=1}^{r} (ns - r + s)\pi_s P_{r-s}/ra_0, \tag{21}$$

where $P_0 = a_0^n$, $a_0 = 1 - p + p\pi_0$ and π_i's are defined in (17).

(ii) G. Binomial-G. Binomial distribution: Here $w(z) = (1-m+mz)^k$. Hence, $\pi_i = m(k - i + 1)\pi_{i-1}/i(1 - m)$, with $\pi_0 = (1 - m)^k$, $a_0 = 1 - p + p\pi_0$ and $P_0 = a_0^n$. The recurrence formula has the same form as in (21).

(iii) G. Binomial-Poisson distribution: Here $w(z) = \exp\{\lambda(z - 1)\}$. Hence, $\pi_i = \lambda^i\pi_0$, $\pi_0 = \exp(-\lambda)$, $a_0 = 1 - p + p\pi_0$ and $P_0 = a_0^n$. The recurrence formula has the same form as in (21). When $n = 1$ and $p\{1 - \exp(-\lambda)\} = \theta$, this was called by A. C. Cohen [1960] an extension of a truncated Poisson distribution.

Type C: Let the distribution of egg masses be a logarithmic distribution with p.g.f. $\log(1 - \lambda z)/\log(1 - \lambda)$. Then the distribution of a larva over the whole field will be $\log\{1 - \lambda w(z)\}/\log(1 - \lambda)$, i.e. the Type *C* distribution with $h(z) = 1 - \lambda w(z)$. The important distributions are obtained by considering $w(z)$ as hypergeometric function G. Binomial, Power-series etc.

Choice of a distribution under the condition of no migration:

Let us suppose that the different sites of a colony are distinct and countable, and let there be no migration between sites of a colony. Assuming the same probabilities of arriving at a particular site by any organism, the distribution of r (when r is fixed) organisms in a particular site is Binomial. Now let us suppose that one or more organisms arriving at the colony follow the truncated Negative Binomial law. (This may be true under the wide applicability of the Negative Binomial in biological data, e.g., Bliss [1953], Evans [1953]). Then, it is easy to show that the p.g.f. of the organisms in a particular site (when there is no migration) is

$$1 - \theta + \theta\{(1 + m_1 - m_1z)^{-k_1} - (1 + m_1)^{-k_1}\}/\{1 - (1 + m_1)^{-k_1}\}$$

where $0 < \theta < 1$, $m_1 > 0$, $k_1 > 0$; i.e. $1 - p + p(1 + m_1 - m_1z)^{-k_1}$ for $0 < p < \{1 - (1 + m_1)^{-k_1}\}^{-1}$, $m_1 > 0$ and $k_1 > 0$. Now suppose that the independent results of n sites are combined together. Then the p.g.f. of the distribution of organisms is

$$[1 - p + p(1 + m_1 - m_1z)^{-k_1}]^n$$

which is a particular case of G. Binomial-G. Binomial. The above distribution can be named as Binomial-Negative Binomial.

5. METHODS OF ESTIMATION FOR G. BINOMIAL-G. BINOMIAL

Here the p.g.f. is $[1 - p + p(1 - m + mz)^k]^n$.

Method of moments: Let $T = K_{[4]}/K_{[2]}^2$, $R = K_{[3]}K_{[1]}/K_{[2]}^2$ and

$S = K_{[1]}^2/K_{[2]}$. The approximate value of n is obtained from

$$n^2(TS - 2R^2 + R) + nS(TS - 6R + 6) + S^2(R - 2) = 0.$$

Then k, m and p are estimated from

$$k = \{S^2 + nS + n^2(2 - R)\}/n\{n(1 - R) - S\},$$

$$m = (nK_{[2]} + K_{[1]}^2)/(k - 1)nK_{[1]} \quad \text{and} \quad p = K_{[1]}/knm. \tag{22}$$

Method of maximum likelihood when n and k are fixed:

Similar to Sprott's results [1958], we have the maximum-likelihood equations as

$$\bar{r} = nk\hat{p}\hat{m} \quad \text{and} \quad L(\hat{m}) = \Sigma a_r G(r) - N = 0 \tag{23}$$

with $L'(\hat{m}) = (d/d\hat{m})L(\hat{m}) = \sum a_r G(r)[\hat{m}^{-1}\{1 - k(1 - \hat{p})^{-1}\} - \{1 + (1 - \hat{m})[\hat{m}k(1 - \hat{p})]^{-1}\hat{m}^{-1}\bar{r}\Delta G(r)\}]$, where $\bar{r}$ is the sample mean, a_r is the frequency at the r-th count, N is the total frequency, $G(r) = (r + 1)\hat{P}_{r+1}/\hat{P}_r\bar{r}$, $\Delta G(r) = G(r + 1) - G(r)$ and $\hat{m}$, $\hat{p}$ are maximum likelihood estimates.

From the first approximate estimates $\hat{p}'$, $\hat{m}'$, the new corrected values $\hat{p}''$, $\hat{m}''$ are estimated from

$$\hat{m}'' = \hat{m}' - \{L(\hat{m}')/L'(\hat{m}')\} \quad \text{and} \quad \hat{p}'' = \bar{r}/nk\hat{m}''. \tag{24}$$

Sample zero frequency when n and k are fixed:

Here the estimates p and m are obtained from

$$a_0 = N[1 - p + p(1 - m)^k]^n \quad \text{and} \quad \bar{r} = nkpm. \tag{25}$$

It may be noted that when $n = 1$, the two equations in (25) are the same as those in (23).

6. EXAMPLE

In order to illustrate how the above discussion can help an experimenter in the field of curve fitting, we fit here Binomial-Negative Binomial to the data in Distribution 1 of MacGuire *et al.* [1957, Appendix]. From the data, the first four factorial cumulants are $K_{[1]} = 2.5900156$, $K_{[2]} = 0.6877630$, $K_{[3]} = 0.0218497$, $K_{[4]} = 0.9080044$.

Hence, on taking $n = 1$, the solution of k, by the method of moments, correct to first decimal place is -12.0. Then the various estimates of m and p are $m = -0.2204963$, $p = 0.9788582$ by the method of zero-cell frequency or maximum-likelihood and $m = -0.2196584$, $p = 0.982591$ by the method of moments.

The fits are shown in Table 1. The fits of other distributions are given along side for reference purposes only.

TABLE 1.

Count per plot	Obs. frequency	Binomial-Neg. Binomial		Negative Binomial [1957]	Poisson; Binomial [1957]	Poisson Power Series[3]
		by M.L. or zero fr.	by method of moments			
0	355	355.000	346.445	324.30	341.84	339.072
1	600	622.478	628.153	660.37	644.37	645.036
2	781	730.994	735.340	734.06	728.03	730.150
3	567	616.306	618.023	610.45	609.14	610.886
4	441	417.545	417.393	408.82	415.60	416.079
5	245	241.296	240.550	236.54	242.72	242.339
6	135	123.567	122.747	122.49	125.17	124.532
7	42	57.406	56.846	58.12	58.20	57.655
8	17	24.632	24.315	25.68	24.76	24.417
9	11	9.395	9.731	10.70	9.75	9.567
10[2]	11	7.301	5.457	4.47	5.42	5.267
χ^2 with ν d.f.		19.184 7.d.f.	20.294 7.d.f.	34.52 8.d.f.	25.52 8.d.f	25.939 8.d.f.

[2]Expected frequencies are from 10 and above

[3]Probabilities are calculated from the p.g.f. $\exp\{-(a+b)+az+bz^2\}$ where $a = 1.9022526$ and $b = 0.3438815$.

7. ASYMPTOTIC EFFICIENCIES

Here we give the asymptotic efficiencies for the various methods of estimation for m and p only in a G. Binomial-G. Binomial distribution.

The determinant of the information matrix up to order N^{-1} for the maximum likelihood estimates m and p is

$$D_{m,p} = N^2n^2[npk\{k(1-p)+(1-m)m^{-1}\}R - \{k(1-p)-1\}^2]/(1-p)^2, \tag{26}$$

where $R = -1 + \sum G^2(r)P_r$ and $G(r) = (r+1)P_{r+1}/nkpmP_r$.

The determinant of the covariance matrix up to order N^{-1} for the moment estimates of m and p is

$$D = (K_2K_4 + 2K_2^3 - K_3^2)/[Nk(k-1)nmK_1]^2, \tag{27}$$

where

$$K_1 = k\,n\,m\,p, \qquad K_2/K_1 = 1 + (k-1)m - (K_1/n),$$

$$K_3/K_1 = 1 + 3(k-1)m + (k-1)(k-2)m^2 - 3(K_2/n) - (K_1^2/n^2)$$

and

$$K_4/K_1 = 1 + 7(k-1)m + 6(k-1)(k-2)m^2 + (k-1)(k-2)(k-3)m^3 - 4(K_3/n) - 6(K_1K_2/n^2) - (K_1^3/n^3) - 3(K_2^2/nK_1).$$

The asymptotic efficiency in the restricted sense is

$$E_1 = 1/D\, D_{m,p}\,. \tag{28}$$

The determinant of the covariance matrix up to order N^{-1} for the sample zero frequency estimates of m and p is

$$D(m,p) = m^2a_0^2\{a_1(1-P_0) - P_0K_1\}/N^2a_2^2n^2K_1P_0\,, \tag{29}$$

where $a_0 = 1 - p + p(1-m)^k$, $a_1 = K_2/K_1$, $P_0 = a_0^n$ and $a_2 = 1 - (1-m)^k - km(1-m)^{k-1}$. The asymptotic efficiency with respect to the method of moments is

$$E_2 = D/D(m,p). \tag{30}$$

It may be noted that $E_2 = E_1^{-1}$ when $n = 1$.

TABLE 2

ASYMPTOTIC EFFICIENCY E_2 RELATIVE TO THE METHOD OF MOMENTS WHEN $n = 1$ AND $k = -1$.

$p\{1-(1-m)^k\} = \theta$	m		
	-0.5	-1	-2
0.3	1.492	1.857	2.193
0.6	1.611	2.125	2.630
0.9	2.444	4.000	4.944

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FURTHER CONSIDERATION OF METHODOLOGY IN STUDIES OF PAIN RELIEF

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INTRODUCTION

In an earlier paper [1] we challenged the prevalent view that in comparisons of pain relieving drugs it is always desirable to have "each patient act as his own control," i.e., to test more than one drug on each patient and to estimate treatment contrasts from within-patient differences. We sought data of other investigators to compare with our own, but we were unable to find references which gave sufficient detail to permit investigation of the merits of alternative designs and analyses. It seemed desirable, therefore, to put our own data on record so as to facilitate discussion of the issues raised. This we did, and the response has been gratifying.

This paper presents and discusses some of the suggestions and comments of those who wrote to us. We are particularly indebted to Frederick Mosteller, Department of Statistics, Harvard University, and to Robert Curnow, A. R. C. Unit of Statistics, University of Aberdeen, Aberdeen, Scotland, who, in addition to making numerous thoughtful comments, performed their own analyses of our data.

A SIMPLE EXTENSION OF THE MODEL

As stated in our earlier paper, this study of relief of post-operative pain was designed as an incomplete block experiment. Each patient was given a dose of a test drug, and the dose was repeated when the patient again complained of severe pain. The number of hours of "greater than 50 percent pain relief" cumulated over both intervals was the measure of drug efficacy. A second drug was tested on each patient in the same way, starting at the time when the patient again complained of severe pain. Three drugs, two levels of a new drug and one level of Demerol, were under study.

It was found that the total hours of relief achieved when a given drug was the second administered was larger on the average than when that drug was administered first. This is consistent with the presumption that the pain decreases with time after operation. However, it invalidates a straightforward least squares analysis based on the model

$$\text{hours of relief} = \text{grand mean} + \text{patient effect} + \text{drug effect} + \text{random error.}$$

We considered the possibility of extending the analysis to include a simple time-period effect, representing the average differences in relief between the second and first periods, but for two reasons we did not pursue it. Firstly, and most importantly, it seemed to us that such a model would be unlikely to be an accurate reflection of the true situation. For example, if the duration of drug effect increases with time after operation, the period effect should be greater when the second drug is given after a potent drug than when it is given after a weak drug. Secondly, our object in the first paper was to compare *simple* alternatives for the design and analysis of studies to evaluate analgesics, and a procedure requiring adjustment for time period as well as patient effects did not seem attractive as a procedure to recommend to clinicians for routine screening of new drugs. (In this connection one should remember that it is almost always necessary to discontinue study of some patients, often for reasons unrelated to drug response. Thus, balance in design is hardly ever achieved.)

Curnow extended the least squares analysis of our data to take account of such a time-period effect. The model becomes

$$\text{hours of relief} = \text{grand mean} + \text{patient effect} + \text{drug effect} + \textit{time period effect} + \text{random error}$$

and the corresponding analysis is given in Table I. He stated that the differences due to the drug which follows a potent one being administered rather later than one which follows a weak one were small and had little effect on the estimates of drug differences. Thus the internal evidence of the experiment itself does not seem to confirm the fears expressed above, and the least squares analysis that includes a time-period effect appears to yield a reasonable description of the data. In particular, in both the inter- and intra-block analyses, the between-group residual mean square is now not larger than the corresponding within-groups mean square.

Curnow went on to point out that the inter-block error is not much larger than the intra-block error, and that one might on this ground justify an analysis *ignoring patient differences*, as shown in Table II.

TABLE I

LEAST SQUARES INTRA-BLOCK ANALYSIS

Source	D.F.	S.S.	M.S.
Blocks	42	607.256	
Periods and Drugs	3	378.015	
Periods ignoring drugs	1	261.628	
Drugs adjusted for periods	2	116.387	58.194
Between Groups Residual	3	3.051	1.017
Within Groups Residual	37	428.945	11.593
Total	85	1417.256	

DRUG COMPARISONS

Comparison	Mean Difference	Variance	t
D vs. T_1	3.421	1.178	3.15
D vs. T_2	2.037	1.061	1.98
T_2 vs. T_1	1.384	1.025	1.35

TABLE II

LEAST SQUARES ANALYSIS IGNORING PATIENT DIFFERENCES

Source	D.F.	S.S.	M.S.
Periods and Drugs	3	434.368	
Periods ignoring drugs	1	261.588	
Drugs adjusted for periods	2	172.780	86.390
Remainder	82	982.888	11.986
Total	85	1417.256	

DRUG COMPARISONS

Comparison	Mean Difference	Variance	t
D vs. T_1	3.548	0.874	3.80
D vs. T_2	1.861	0.831	2.04
T_2 vs. T_1	1.687	0.816	1.87

This observation suggests that in future experiments conducted under similar conditions we should *not* arrange matters to eliminate patient effects, if it will cost us much to do so.

Our own calculations and scatter diagrams confirm Curnow's results. However, in view of our first argument against the use of a simple time-period effect we found them surprising and made some further investigation. We take note first that the fact that a model "fits", in the sense that certain internal checks are satisfied, does not insure its correctness. If, for example, second-dose relief were more variable than first-dose relief, an examination of residuals would not in this case establish that fact; the estimated first-dose residual for a given patient has precisely the same magnitude as the estimated second-dose residual for that patient when we use the present model. The second-dose relief scores are, in fact, more variable than are those for first doses. This may be observed by examination of Table 1b in [1] and it is reflected in the fact that the *within patient* residual variance (Table 3a), which excludes the component of variability due to patient differences, is actually larger than the *between patient* variance for first dose relief (Table 2).

If the facts are in accord with the assumption that the increment in relief with increasing time after administration is proportional to time after operation, the effect of the model having only a simple time-period effect would be to assign a part of the drug difference to the time-period effect and thus to reduce the measured differences between drugs, as compared to an analysis for the first period only. In fact, the difference between the most and least potent drugs (D and T_1) estimated by use of the extended model is less by about 15 percent than the estimate obtained from analysis of the first period only.

Granted, then, that the model with a simple time-period effect fits the data insofar as intra-block checks are concerned, what may we expect to gain or lose if we go ahead and use it? We do have some evidence which tends to contradict the assumptions of this model, but the effects do not seem large. We have some slight evidence that we may lose discriminating power by misinterpreting drug differences as time-period effects, but, as judged from these data, the reduction in variance may well compensate. Insofar as testing (i.e., deciding which drug is better) is concerned, or estimating potency in an experiment with a full range of standards, the analysis based on this model should give essentially valid results.

In any event, apart from the question of the best analysis for these data, the smallness of the between patients component in the extended analysis suggests that we would have achieved at least equal precision

for drug comparisons if we had kept each patient on a single drug throughout the experimental period. Had we done so, we would have had, in addition to possible benefits in precision, the comfort of closely imitating the ordinary clinical situation, and the advantage of an unbiased estimate of a clearly interpretable measure of effectiveness along with an unbiased estimate of its variance. We might also have had the cooperation of several more surgeons, some of whom, understandably, object to studies which require administration of several coded drugs to each patient.

A REGRESSION MODEL

In furtherance of the point of view that the cost of statistical work is generally small compared to the cost of gathering clinical data, Mosteller suggested that the data be analyzed in accordance with a model which might give a fairly realistic appraisal of the time-trend effect. In particular, he suggested that we not cumulate the two doses of each drug but analyze the data for single doses according to the following model.

$$y_{imd} = \alpha_i + \beta_m + \gamma_m t_{imd} + \epsilon_{imd} ,$$

where

α_i = effect of i-th subject,
β_m = effect of medication m when given at time zero,
γ_m = regression of effect of medication m on time of administration,
t_{imd} = time at which individual i receives the d-th dose of medication m,
ϵ_{imd} = random error.

This analysis was carried out, using the times of drug administration (not shown, but available upon request) in addition to the data already presented. It was found that the regression coefficients γ_m were quite close to one another and, if we restrict the model to the case of equal γ_m, the least squares estimate of this common value is 0.20, corresponding to an additional hour of drug relief for every five hour interval between operation and drug administration. Using this restricted model and doubling the estimated effects to make these results comparable to those for our other analyses, we have the estimates of treatment differences shown in Table III.

Assuming for now the correctness of the regression model, we see that these estimates are quite close to those obtained in the analysis using only the first drug for each patient—Table 2 of [1]. However, the variances are reduced by about one-third, so that the regression

TABLE III

DRUG COMPARISONS FROM REGRESSION MODEL ANALYSIS

Comparison	Mean Difference	Variance	t
D vs. T_1	4.066	0.824	4.48
D vs. T_3	2.530	0.732	2.96
T_3 vs. T_1	1.534	0.708	1.82

analysis, using all the data, appears to have about 50 percent greater precision than the "first drug only" analysis, which uses only half the data.

Comparing the apparent precisions provided by the above analyses, we see that Curnow's intra-block analysis, adjusting for patients and time periods (Table I) appears comparable in precision to the "first drug only" analysis. Curnow's analysis ignoring patient effects (Table II) appears almost equal in precision to the analysis based on the regression model.

OTHER COMMENTS AND ERRATA

A third correspondent, Irwin Bross, Roswell Park Memorial Institute, Roswell Park, New York, raised several points, in part overlapping those above. In addition he pointed out that the results of the "least squares" analysis (Table 4a in [1]) differ appreciably from the analysis based on simple linear combinations of intra-individual contrasts. Since the design is nearly balanced, closer agreement might be expected, even though our "least squares" analysis fails to allow for time-period effects. In fact, contrary to the suggestion in [1], the "linear combinations" analysis is not really comparable to the "least squares" analysis. The reason is that in estimating, say, $D - T_1$, no account was taken of the information about this difference given by contrasting the direct estimate of $D - T_3$ with the estimate of $T_1 - T_3$. If we take an average of the directly observed difference, $D - T_1$, with the contrast obtained by combining $D - T_3$ with $T_1 - T_3$, weighting inversely as the estimated variances, and proceed similarly for the other comparisions, we get Table IV, which agrees much more closely with the "least squares" analysis (Table 4a in [1]). As might be expected, the "extended least squares" analysis which does allow for time-period effects (Table I) gives results in excellent agreement with Table IV.

This revision leads in turn to a more precise combined intra- and inter-block analysis in place of that shown in Table 3c in [1]. The result (not given) is quite close to the "least squares" combined analysis.

TABLE IV

DRUG COMPARISONS FROM ANALYSIS OF WITHIN PATIENT CONTRASTS

Comparison	Mean Difference	Variance	t
D vs. T_1	3.449	1.206	3.18
D vs. T_2	2.051	1.073	1.98
T_2 vs. T_1	1.398	1.031	1.38

Both Curnow and Bross pointed out that erroneous entries are shown in Table 4c in [1]. This table should be replaced with Table 4c (revised) as shown.

TABLE 4c (revised)

COMBINED INTRA- AND INTER-BLOCK ANALYSIS FOR DRUG DIFFERENCES

$$w = \frac{1}{1.174} = 0.8518 \qquad w' = \frac{1}{3.720} = 0.2688$$

Calculation of Average Mean Difference: Drug D vs. Drug T_1

$$\frac{(w)(3.150) + (w')(3.900)}{w + w'} = 3.330.$$

Calculation of Variance of Difference

$$\frac{1}{w + w'} = \frac{1}{0.8518 + 0.2688} = 0.892.$$

DRUG COMPARISONS

Comparison	Mean Difference	Variance	t
D vs. T_1	3.330	0.892	3.52
D vs. T_2	1.843	0.848	2.00
T_2 vs. T_1	1.442	0.828	1.58

DISCUSSION

The point which we wished to emphasize in [1] was that on account of the increase in duration of relief with time of administration, the use of simple intra-patient contrasts—"each patient his own control"—may not be optimal, and that an experiment in which each patient received only a single drug might be preferable.

The analyses proposed by Curnow and Mosteller have demonstrated that for this data a model taking account explicitly of the effect of time of drug administration will yield more efficient estimates than does the one-way analysis of the first period only. With respect to the analysis of the present data, both the Curnow and Mosteller models appear to fit quite well, and the estimates of the drug effects produced by their analyses are more precise than those derived from the analysis for the first period only.

It is not clear, however, whether the above finding should be construed as evidence supporting the need for more complex models and analyses than are currently in vogue, or whether instead it is evidence supporting our original viewpoint. If, as the evidence of Curnow's analysis suggests, patient differences are negligible, we would have no reason at all to use each patient as his own control. Were each patient given only one drug, the time-period effect of Curnow's model would be eliminated from treatment contrasts and the one-way analysis—using now the whole of the data—should be fully efficient.

Even if patient differences are not negligible, the advantages of simplicity, both of design and analysis, may outweigh a small gain in efficiency which could be achieved with the use of a more complex design and analysis. With our data, for example, the estimates of greatest apparent precision were those provided by the regression model, and the gain in precision compared to the analysis of the first period only was 50 percent. Such a gain is, of course, quite worth having, but it is not overwhelming, and it is easy to believe that had our design assigned one drug to each patient throughout the period of study, the one-way analysis might have equalled the present regression analysis in precision.

In conclusion, we must again emphasize that we do not claim that our findings apply to all kinds of pain studies. There may be many situations for which within-patient contrasts are far superior to between-patient contrasts. What we do claim is that no principal such as "each patient his own control" is entitled to the status of dogma. In some situations, at least, the simpler methods are better.

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FITTING A GEOMETRIC PROGRESSION TO FREQUENCIES

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SUMMARY

This paper discusses the interpretation of frequency data when the series of observed frequencies is assumed to arise from a population in which the expected frequencies form a geometric progression. Such situations occur in the study of steadily increasing insect populations and similar phenomena, where the common ratio of frequencies is related to the rate of growth of the population.

The estimation of the common ratio, and tests for the significance of departure from geometric trend, are discussed. Asymptotic formulae for the tail probabilities in large samples are determined.

The methods and tests of significance are illustrated by application to some experimental data.

I. INTRODUCTION

Observations are often recorded by classifying them into several classes and counting the frequencies of occurrence in each class. In general, the expected frequencies will be partly specified by theoretical considerations, but will often also depend on one or more unknown parameters.

The interpretation of such data then involves, firstly, testing its concordance with the assumed form of expected frequencies, and secondly, estimating the unknown parameters. Thus, for instance, in a steadily increasing population of organisms, the number of individuals expected in successive age-groups will be in geometric progression, the common ratio between the expected numbers representing not only the growth of the population but also the effects of mortality, migration and other factors. In such a study, one of the objects would be to test the concordance with the assumed geometric progression, and the other would be to estimate the common ratio accurately.

In general problems of this kind, the parameters may be estimated, and the accuracy of the estimates assessed, by the method of maximum likelihood. To test the fit of the model to the data, the χ^2 test is generally

appropriate. If hypothetical values of the parameters have been specified, as occurs in many practical instances, their concordance with the estimates derived from the data can also be tested by means of χ^2.

In the particular case, with which this paper deals, of expected frequencies in geometric progression, there exist sufficient statistics for the two parameters involved, representing the general level of the frequencies and their geometric trend. This facilitates estimation and significance testing, although, since the equations of estimation are in general non-linear, iterative methods are required in the arithmetical work of calculating estimates.

The need to fit frequencies in this way arose from a method, devised by Dr. R. D. Hughes, Division of Entomology, C.S.I.R.O., of using the age distribution in an aphid population to study its rate of growth in the field. The device of using the proportions of individuals in the immature instars in a field population of aphids to give, firstly, the age distribution, and secondly, the rate of increase of the population, is the subject of a forthcoming paper by Hughes. In the present paper, some preliminary observations of instar distribution under controlled experimental conditions are discussed.

Chapman and Robson [1960] have considered the age distribution in a stationary population subject to constant mortality. As this formulation leads to a geometric progression of expected frequencies, many of their results anticipate results given in this paper. However, the general objects and scope of the two papers are different.

Aphid populations under uniform and favourable conditions increase at a constant rate, so that their expected numbers at equal intervals of time form a geometric progression. However, the numbers even of an initially small population quickly become too large to be counted accurately. An estimate of the rate of growth of the population may then be made from the age distribution. The immature aphid passes through four instars before reaching maturity. In a stationary population, the number expected in each instar is proportional to its duration. For some species of aphids, for instance *A. craccivora*, the average durations of the first three instars are probably equal under constant conditions, so that equal numbers will be expected in each instar in a stationary population. When the population is increasing at a constant rate, the numbers in each instar will approximate to a geometric progression.

If the common duration of each of the first three instars is c, and the growth-rate of the population is ρ, then the ratio of the number in each instar to that in the preceding one is approximately

$$e^{-c\rho}.$$

In this result, mortality has been neglected, since it has been shown that under favourable conditions mortality in the immature stages is negligible.

By taking a random sample from the aphid population and determining the number in each instar we can first check the validity of the assumption of uniform growth by testing whether the numbers are consistent with a geometric progression. Having satisfied ourselves on this point, we can then estimate the common ratio of the numbers. If c, the duration of each instar, is known, the growth-rate can then be determined.

If the durations of the different instars are different, the above method will be modified, and the estimation of the growth-rate is a little more complicated; in principle, however, such data will still provide information from which the growth-rate can be determined.

II. THE BASIC DISTRIBUTION

We consider a sample of N individuals classified into k classes, the observed frequency in class i being n_i, with expected value

$$E(n_i) = \lambda\mu^i \qquad (i = 0, 1, \cdots, k-1).$$

If N is assumed to have a Poisson distribution, so has each of the n_i; the joint probability density is then

$$P(n_0, n_1, \cdots, n_{k-1}) = \prod (e^{-\lambda\mu^i}\lambda^{n_i}\mu^{in_i}/n_i\,!) = \frac{e^{-\lambda\phi_0(\mu)}\lambda^N\mu^T}{n_0\,!\,n_1\,!\cdots n_{k-1}\,!}, \quad (1)$$

where

$$T = n_1 + 2n_2 + \cdots + (k-1)n_{k-1},$$

and

$$\phi_0(\mu) = 1 + \mu + \cdots + \mu^{k-1}.$$

From the form of the density it is apparent that N and T are a pair of sufficient statistics for the parameters λ and μ. Thus, questions of estimation may be referred to the joint distribution of N and T.

By summing the probability (1) over values of the n_i leading to the given values of N and T, we find the joint distribution of N and T as

$$P(N, T) = \frac{C(N, T)}{N!}\, e^{-\lambda\phi_0(\mu)}\lambda^N\mu^T, \quad (2)$$

where $C(N, T)$ is a numerical coefficient.

The number N has a Poisson distribution with mean $\lambda\phi_0(\mu)$;

$$P(N) = e^{-\lambda\phi_0(\mu)}[\lambda\phi_0(\mu)]^N/N!.$$

Hence for given N, the conditional density of T, which is independent of λ, is

$$P(T \mid N) = C(N, T)\mu^T/[\phi_0(\mu)]^N.$$

This is a special case of the distribution discussed by Noack [1950] and described by him as a power-series distribution. Our $[\phi(\mu)]^N$ takes the place of his $f(z)$. From this expression for the density we see that $C(N, T)$ is the coefficient of μ^T in $\phi_0(\mu)^N$. This fact enables the numerical coefficient to be determined directly.

This conditional density of T provides the basis for estimates and tests of significance about μ.

III. THE COMBINATORIAL FACTOR

The coefficient $C(N, T)$ is seen to be a generalization of the binomial coefficient (for the positive binomial, when $k = 2$; for the negative binomial, when $k = \infty$). It is the number of ways of allocating T like objects among N different cells, none of which may contain more than $k - 1$ objects (see Riordan [1958], page 104, where some recurrence relations and moment formulae are also given).

The coefficients are generated by the function

$$[\phi_0(\mu)]^N = \left(\frac{1-\mu^k}{1-\mu}\right)^N = \left[\sum \binom{N+i-1}{N-1}\mu^i\right]\left[\sum \binom{N}{j}(-\mu^k)^j\right].$$

On equating coefficients of μ^T we find

$$C(N, T) = \binom{N+T-1}{N-1} - \binom{N}{1}\binom{N+T-k-1}{N-1} + \binom{N}{2}\binom{N+T-2k-1}{N-1} - \cdots \qquad (3)$$

The series has $1 + [T/k]$ terms. This expansion in terms of binomial coefficients is useful, especially if k is large, since the first few terms then give a close approximation.

Because of symmetry, $C(N, T) = C[N, (k-1)N - T]$ so that results for $T > \frac{1}{2}(k-1)N$ can be found from those for $T < \frac{1}{2}(k-1)N$.

From the generating function or otherwise we may also deduce the recurrence relation

$$C(N, T) = C(N, T-1) + C(N-1, T) - C(N-1, T-k)$$

which is useful for computation.

Hitherto we have been considering relations among the $C(N, T)$ for a fixed value of k. We now consider relations for different k, and shall indicate by a suffix the number of classes.

We may express the coefficients for k classes in terms of the coefficients corresponding to the factors of k, by means of the following reduction formula.

If $k = fg$,

$$\phi_{0k}(\mu) = \frac{1-\mu^k}{1-\mu} = \frac{1-\mu^f}{1-\mu} \cdot \frac{1-\mu^{fg}}{1-\mu^f} = \phi_{0f}(\mu) \cdot \phi_{0g}(\mu^f).$$

Hence

$$C_k(N, T) = C_f(N, T) + C_f(N, T - f)C_g(N, 1) + C_f(N, T - 2f)C_g(N, 2) + \cdots,$$

a series of $1 + [T/f]$ terms. The terms of these series are all positive, and generally smaller than those of the series (3) of products of binomial coefficients. They may have some advantages for computation, provided the coefficients for f and g classes are known.

By differentiating the generating function with respect to its parameter we may prove recurrence formulae of the type

$$C(N, T) = \frac{N}{(k-1)N - 2T} \cdot [(k-1)C(N-1, T) + (k-3)C(N-1, T-1) + \cdots - (k-1)C(N-1, T-k+1)]. \tag{4}$$

When $k = 3$, many particularly simple recurrence formulae may be established. Recurrence relations when $k = 3$ are

$$C(N, T) = \frac{N}{T(2N-T)} \cdot [(2N-1)C(N-1, T-1) + 3(N-1)C(N-2, T-2)]$$

$$= \frac{1}{2T}[(2N - T + 1)C(N, T-1) + 3NC(N-1, T-2)]$$

$$= \frac{N}{N-T}[C(N-1, T) - C(N-1, T-2)],$$

the last being a particular case of (4). As k increases the recurrence formulae become more complicated.

IV. MOMENTS OF THE CONDITIONAL DISTRIBUTION OF T

The moments and cumulants of the conditional distribution of T are of general interest, and will also be of use when the determination of probabilities in the tails of the distribution is being considered.

Since the cumulants for a sample of N are simply N times those for a sample of 1, we shall consider a sample of 1, for which T equals X, the number of the class $(0, 1, \cdots, k-1)$ in which the observation falls.

Clearly, if

$$\phi_r(\mu) = \left(\mu \frac{d}{d\mu}\right)^r \phi_0(\mu) = \sum_{x=0}^{k-1} x^r \mu^x,$$

then the rth moment about zero is $\phi_r(\mu)/\phi_0(\mu)$. This result is equivalent to the results of Noack [1950], though expressed in a slightly different manner.

However, unless k is small, these expressions are not convenient for the computation of the central moments and cumulants, which are more simply found directly,

The moment-generating function of X is

$$E(e^{sX}) = \sum \mu^x e^{sx} / \sum \mu^x = \phi_0(\mu e^s)/\phi_0(\mu).$$

Thus the cumulant-generating function is

$$\begin{aligned} K(s) &= \log \phi_0(\mu e^s) - \log \phi_0(\mu) \\ &= -\log(1 - \mu e^s) + \log(1 - \mu^k e^{sk}) + \log(1 - \mu) - \log(1 - \mu^k) \\ &= \sum \frac{\mu^r}{r}(e^{rs} - 1) - \sum \frac{\mu^{rk}}{r}(e^{rsk} - 1). \end{aligned}$$

From this expansion we derive the particular results

$$\kappa_1 = \frac{\mu}{1-\mu} - \frac{k\mu^k}{1-\mu^k},$$

$$\kappa_2 = \frac{\mu}{(1-\mu)^2} - \frac{k^2\mu^k}{(1-\mu^k)^2},$$

$$\kappa_3 = \frac{\mu + \mu^2}{(1-\mu)^3} - \frac{k^3(\mu^k + \mu^{2k})}{(1-\mu^k)^3},$$

$$\kappa_4 = \frac{\mu + 4\mu^2 + \mu^3}{(1-\mu)^4} - \frac{k^4(\mu^k + 4\mu^{2k} + \mu^{3k})}{(1-\mu^k)^4}.$$

The form of the cumulant-generating function shows that, if u_k is a geometric variable with parameter μ^k, then $X + ku_k = u_1$. It also follows that, if $u_k(N)$ is a negative binomial variable with parameter μ^k and index N, then $T + ku_k(N) = u_1(N)$.

When $\mu = 1$, the distribution is the uniform discrete distribution, and the cumulants are expressible in terms of Bernoulli's numbers. We then have

$$K(s) = -\log\left(\frac{e^s - 1}{s}\right) + \log\left(\frac{e^{sk} - 1}{sk}\right)$$

$$= \frac{k-1}{2}s + (k^2 - 1)\frac{B_2}{2}\frac{s^2}{2!} + (k^4 - 1)\frac{B_4}{4}\frac{s^4}{4!} + \cdots,$$

where $s/(e^s - 1) = 1 + \sum B_r s^r/r! = e^{Bs}$ in symbolic form. Hence $\kappa_r = (k^r - 1)B_r/r$; in particular, $\kappa_1 = (k-1)/2$, $\kappa_2 = (k^2 - 1)/12$, $\kappa_3 = 0$, $\kappa_4 = -(k^4 - 1)/120$.

Relation between Cumulants Corresponding to μ and μ^{-1}.

When the series of frequencies is reversed, the ratio μ is replaced by its reciprocal. It therefore follows that, when μ is replaced by μ^{-1}, the odd cumulants other than κ_1 are simply changed in sign, and the even cumulants are unaffected. We have

$$\kappa_1(\mu^{-1}) = k - 1 - \kappa_1(\mu),$$

$$\kappa_r(\mu^{-1}) = (-1)^r\kappa_r(\mu) \qquad (r > 1).$$

These results may also be readily verified from the form of the cumulant-generating function.

Because of these facts, we need not consider values of μ outside the range (0, 1).

V. ESTIMATION OF THE RATIO OF FREQUENCIES

In the conditional distribution, T is a sufficient statistic for the parameter μ, the common ratio of the expected ferquencies. Thus the estimation of μ is straightforward. However, since the equation of estimation by the method of maximum likelihood is non-linear, iterative methods will be required to solve it.

The logarithm of the conditional probability of T, apart from terms independent of the parameter, is $L = T \log \mu - N \log \phi_0(\mu)$, and its first derivative with respect to μ is

$$(T/\mu) - (N\phi_1/\mu\phi_0). \tag{5}$$

Equating the derivative to zero gives the maximum likelihood estimator of μ. We indicate by an asterisk the maximum likelihood estimator and functions of it. Thus

$$T - (N\phi_1^*/\phi_0^*) = 0. \tag{6}$$

Since the equation is linear in T, it is clear that the estimator is to be found simply by equating T to its expectation: $T = N\kappa_1^*$, as may be verified from the results of the previous section.

The variance of the derivative (5) gives the information I_μ about μ in the sample. Being linear in T, the derivative has variance

$$V(T)/\mu^2 = N\kappa_2/\mu^2 = \frac{N}{\mu^2}\left(\frac{\mu}{(1-\mu)^2} - \frac{k^2\mu^k}{(1-\mu^k)^2}\right) = I_\mu .$$

This result is a special case of the results of Patil [1961], who investigates the estimation of the parameter of a generalized power-series distribution. In large samples, the reciprocal of I_μ approximates the variance of the estimate μ^*; that is, $V(\mu^*) = \mu^2/N\kappa_2$.

For purposes of calculating and tabulating the solutions of the maximum likelihood equation, we shall put

$$T/(k-1)N = v,$$

so that, for all k, $0 \leq v \leq 1$.

Then the estimating equation may be written

$$\kappa_1 = \frac{\mu}{1-\mu} - \frac{k\mu^k}{1-\mu^k} = (k-1)v. \tag{7}$$

An alternative form is

$$\frac{1}{1-\mu} - \frac{k}{1-\mu^k} = -(k-1)(1-v),$$

or

$$\frac{\mu^{-1}}{1-\mu^{-1}} - \frac{k\mu^{-k}}{1-\mu^{-k}} = (k-1)(1-v).$$

Thus, if μ^* is the root corresponding to v, then μ^{*-1} is the root corresponding to $1-v$. In particular, if $v = \frac{1}{2}$, $\mu^* = 1$.

Since the roots corresponding to values of v exceeding $\frac{1}{2}$ are the reciprocals of roots corresponding to values of v less than $\frac{1}{2}$, we may henceforth confine attention to $v \leq \frac{1}{2}$, $\mu \leq 1$.

Equation (7) can be solved iteratively, once an approximate value of μ has been chosen. If v is not too near $\frac{1}{2}$, and k is not small, a first approximation is

$$\mu_1 = \frac{(k-1)v}{1+(k-1)v} = \frac{T}{T+N}, \tag{8}$$

and a second approximation is

$$\mu_2 = \mu_1 + k\mu_1^k(1-\mu_1)^2.$$

The difference between the two sides of (7) when an approximate value of μ is substituted represents $-\mu/N$ times (5), the first derivative

of the likelihood. The adjustment to μ is given by the ratio of this difference to $-\mu I_\mu/N$. Then, approximately,

$$\mu^* = \mu\left[1 - \frac{\kappa_1 - (k-1)v}{\kappa_2}\right].$$

The substitution and adjustment may be repeated as often as required to give the desired accuracy.

If v is close to $\frac{1}{2}$, an approximation alternative to (8) is to be preferred. We put

$$\mu = e^{-\theta}, \qquad v = \tfrac{1}{2} - w.$$

Then equation (7) becomes

$$\frac{e^{-\theta}}{1 - e^{-\theta}} - \frac{ke^{-k\theta}}{1 - e^{-k\theta}} = (k-1)(\tfrac{1}{2} - w)$$

or, symbolically in terms of Bernoulli's numbers,

$$\frac{1}{\theta}(e^{B\theta} - e^{Bk\theta}) = (k-1)(\tfrac{1}{2} - w).$$

We then find

$$\frac{B_2\theta}{2!}(k^2 - 1) + \frac{B_4\theta^3}{4!}(k^4 - 1) + O(\theta^5) = (k-1)w,$$

whence

$$\theta = \frac{12w}{k+1} + \frac{144}{5}\frac{(k^2+1)w^3}{(k+1)^3} + O(w^5),$$

and

$$\mu^* = 1 - \frac{12w}{k+1} + \frac{72w^2}{(k+1)^2} - \frac{144}{5}\frac{(k^2+11)w^3}{(k+1)^3} + O(w^4). \qquad (9)$$

Solutions of the maximum likelihood equation for various values of k and v are given in Table 1. Once values of μ are given, it is easy to compute I_μ. As we shall see in Section X, the solution not only gives a point estimate of the ratio μ, and an approximate standard error based on the information function I_μ, but also gives a means of determining tail probabilities, needed in making significance tests and setting confidence limits.

VI. ESTIMATION OF λ

In general, for the problems considered in this paper, the actual value of λ, representing the size of the population (or rather, of the

TABLE 1

MAXIMUM LIKELIHOOD ESTIMATE OF μ [WITH ARGUMENT $v = T/(k-1)N$]

k	2	3	4	5
0.00	0	0	0	0
0.05	052632	092894	131334	167119
0.10	111111	178395	238358	291010
0.15	176471	261940	333333	392939
0.20	250000	346500	422530	483323
0.25	333333	434259	509668	567737
0.30	428571	527202	597388	649654
0.35	538462	627431	687922	731617
0.40	666667	737405	783468	815815
0.45	818182	860221	886484	904443
0.50	1.000000	1.000000	1.000000	1.000000

zero-class), is not of interest. However, for testing the significance of departure of the frequencies from a geometric progression, estimates of the expected frequencies in each class will sometimes be required. We shall then be interested in the simultaneous estimation of λ and μ, based on N and T. We therefore consider this question, rather than the estimation of λ alone.

The joint probability of N and T, as given in (2), is

$$\frac{C(N, T)}{N!}\, e^{-\lambda\phi_0(\mu)}\lambda^N\mu^T,$$

so that the logarithm of the likelihood, considered as a function of the two parameters, and with constant factors ignored, is $L = -\lambda\phi_0(\mu) + N \log \lambda + T \log \mu$. The derivatives are

$$\begin{aligned} L_\lambda &= -\phi_0(\mu) + (N/\lambda), \\ L_\mu &= [-\lambda\phi_1(\mu) + T]/\mu. \end{aligned} \tag{10}$$

The estimates are given when these derivatives are equated to zero, or when N and T are equated to their expected values. For direct solution, λ can be eliminated between the two equations, giving an equation for μ identical with (6). μ having been found, λ may then be found by substitution in (10).

For simultaneous solution, and also to give a measure of the information about λ and μ, we require the covariance matrix of the derivatives. Noting that N is a Poisson variate, with variance equal to its mean $\lambda\phi_0(\mu)$, that the covariance of N and T is $\lambda\phi_1(\mu)$ and that the

variance of T is $\lambda\phi_2(\mu)$, we find for the covariance matrix of the derivatives

$$\mathbf{I} = \lambda\begin{bmatrix} \phi_0/\lambda^2 & \phi_1/\lambda\mu \\ \phi_1/\lambda\mu & \phi_2/\mu^2 \end{bmatrix}.$$

The inverse of $\mathbf{I}$, giving approximate variances and covariance of the estimates in large samples, is

$$\mathbf{I}^{-1} = \frac{1}{\lambda(\phi_0\phi_2 - \phi_1^2)}\begin{bmatrix} \lambda^2\phi_2 & -\lambda\mu\phi_1 \\ -\lambda\mu\phi_1 & \mu^2\phi_0 \end{bmatrix}.$$

From trial values λ, μ of the parameters we find improved estimates by means of the equations

$$\begin{bmatrix} \lambda^* \\ \mu^* \end{bmatrix} = \begin{bmatrix} \lambda \\ \mu \end{bmatrix} + \mathbf{I}^{-1}\begin{bmatrix} L_\lambda \\ L_\mu \end{bmatrix},$$

which give explicitly

$$\begin{aligned} \lambda^* &= \frac{N\phi_2 - T\phi_1}{\phi_0\phi_2 - \phi_1^2}, \\ \mu^* &= \mu\left[1 - \frac{N\phi_1 - T\phi_0}{\lambda(\phi_0\phi_2 - \phi_1^2)}\right]. \end{aligned} \tag{11}$$

Note that the trial value of λ does not appear in the equation for λ^*, since the estimating equations are linear in λ^*. The adjustments given by (11) may be repeated to give the accuracy required.

The expected frequency in class i is $\lambda\mu^i$; the variance of the estimated frequency may be determined, using $\mathbf{I}^{-1}$, as

$$\frac{\lambda\mu^{2i}}{\phi_0\phi_2 - \phi_1^2}(\phi_2 - 2i\phi_1 + i^2\phi_0).$$

The relative variance of the estimated frequency is therefore

$$\frac{\phi_2 - 2i\phi_1 + i^2\phi_0}{\lambda(\phi_0\phi_2 - \phi_1^2)}.$$

VII. TESTS OF DEPARTURE FROM PROPORTIONALITY

Before any use is made of data to which proportional frequencies have been fitted, it is necessary to test whether the observations depart significantly from the estimated frequencies.

Following Cochran [1954], we shall denote by X^2 the statistic used for testing the discrepancy between observed and expected frequencies, and by χ^2 the random variable with the familiar distribution, to which the distribution of X^2 approximates. We consider here the adequacy

of the χ^2-approximation in testing X^2 for departure from expectation in the present problem.

Alternatively, we may use the fact that, because N and T are sufficient for λ and μ, the probability of a sample, conditional on N and T, is independent of the parameter values. An exact conditional test can thus be made, provided there are several possible samples corresponding to the given values of N and T. The probability of a sample of values $n_0, n_1, \cdots, n_{k-1}$ with $\sum n_i = N$ and $\sum i n_i = T$ is

$$\frac{1}{\prod (n_i\,!)} e^{-\lambda\phi_0(\mu)} \lambda^N \mu^T.$$

Likewise the joint probability of N and T is

$$\frac{C(N, T)}{N!} e^{-\lambda\phi_0(\mu)} \lambda^N \mu^T,$$

where $C(N, T)$ is as defined in (2). Hence, the probability of the sample conditional on N and T is

$$\frac{N!}{C(N, T) \prod (n_i\,!)}. \tag{12}$$

By enumerating all possible samples and their probabilities we can decide the significance of an observed sample. Often the set of samples deemed to show significant departure from proportionality will be taken as a set of the samples with the smallest probabilities; however, in many problems, other criteria may be considered more appropriate. The use of X^2 has the advantage that it orders the samples according to a quantitative measure of departure from proportionality, whereas the probability attaching to a particular sample may be small merely because of the discontinuity of the distribution. A satisfactory arrangement would therefore be to order the samples by means of X^2, but to use the exact probabilities. In many cases the exact cumulated probabilities will not differ much from those given by the χ^2-distribution. The questions of calculation of probabilities and of choice of the significant set have been thoroughly discussed by Fisher [1950].

As an example of the exact calculation, we consider the following data in four classes:

	Observed	Expected
n_0	30	27
n_1	5	9
n_2	2	3
n_3	3	1

It will be seen that, because the numbers are restricted to four classes, the possibilities are much fewer in number than in other examples, such as that of the testing of deviations from a Poisson distribution, as discussed by Fisher. For this set, $N = 40$, $T = 18$, and it is readily verified that $\mu^* = \frac{1}{3}$, $\lambda^* = 27$. X^2 is easily calculated as

$$\frac{n_0^2}{27} + \frac{n_1^2}{9} + \frac{n_2^2}{3} + \frac{n_3^2}{1} - N = 6.444;$$

however, since the expected values in two of the classes are small, the tabulated distribution of χ^2 is not likely to be a good approximation to the distribution of X^2 for this sample. For this reason, as an example of method, the exact probabilities have been determined for the 37 possible samples having values $N = 40$, $T = 18$. The probabilities and the values of X^2 are given in Table 2.

We have $C(40, 18) = 220{,}495{,}831 \times 10^6$.

From the Table it is seen that the sample in question just attains significance at the 5 percent level; this is so whether the samples are ordered according to their probability or by X^2. The tabulated distribution would give a probability, for χ^2 with two degrees of freedom,

$$e^{-\frac{1}{2}X^2} = e^{-3.222} = 0.039866.$$

This shows that, for this example, the tabulated distribution underestimates the significance probability only slightly. On the other hand, for the sample

31 3 3 3

for which the probability accumulated according to X^2 is 0.008190,

$$X^2 = 8.593,$$

the probability of exceeding which is

0.013619.

The probability here is overestimated somewhat.

As a matter of interest, the mean and variance of for the distribution generated by this set are $E(X^2) = 1.9956$, $V(X^2) = 3.4223$, compared with the values of 2 and 4 respectively for the χ^2-distribution. The low variance will usually lead to overestimation of probabilities at the tails of the distribution and underestimation of significance, when referred to χ^2, though this effect will sometimes be masked by local irregularities of the distribution.

VIII. MOMENTS OF THE NON-PARAMETRIC DISTRIBUTION

We now show how the moments of the exact distribution of X^2

TABLE 2.

THE FREQUENCIES IN FOUR CLASSES FOR WHICH $N = 40$, $T = 18$

n_0	n_1	n_2	n_3	Probability	Cumulative probability	$27\ \chi^2$
34	0	0	6	.000000	.000000	1048
31	0	9	0	.000001	.000001	610
33	0	3	4	.000003	.000004	522
33	1	1	5	.000004	.000008	696
32	0	6	2	.000010	.000018	376
32	3	0	5	.000019	.000037	646
31	1	7	1	.000089	.000126	352
32	1	4	3	.000098	.000224	334
32	2	2	4	.000146	.000370	424
30	2	8	0	.000173	.000543	408
22	18	0	0	.000514	.001058	376
31	4	1	4	.000781	.001839	370
30	6	0	4	.000807	.002646	360
31	2	5	2	.000938	.003584	226
31	3	3	3	.002083	.005667	232
30	3	6	1	.003229	.008896	198
29	4	7	0	.003460	.012356	250
24	15	0	1	.004561	.016917	198
28	9	0	3	.005574	.022491	190
23	16	1	0	.006841	.029332	226
26	12	0	2	.009578	.038910	136
30	5	2	3	.009688	.048598	174
30	4	4	2	.012110	.060708	120
29	7	1	3	.013840	.074547	160
28	6	6	0	.023412	.097959	136
29	5	5	1	.029063	.127022	88
24	14	2	0	.034206	.161228	120
25	13	1	1	.038311	.199539	88
27	10	1	2	.046824	.246363	66
29	6	3	2	.048439	.294802	58
27	8	5	0	.070236	.365038	66
28	8	2	2	.075253	.440291	40
25	12	3	0	.083006	.523297	58
28	7	4	1	.100337	.623634	22
26	10	4	0	.105354	.728988	40
26	11	2	1	.114932	.843920	22
27	9	3	1	.156080	1.000000	0

may be determined. This distribution is independent of the population parameters, and depends only on the values of N and T.

We consider first the conditional moments of the n_i. From expression (12) we see that

$$\frac{C(N, T)}{N!} = \sum \frac{1}{\prod (n_i\ !)},$$

where the sum is taken over all sets of the n_i such that $\sum n_i = N$ and $\sum i n_i = T$. Now the expected value of n_j is

$$\frac{N!}{C(N, T)} \sum \frac{n_j}{\prod (n_i\ !)}.$$

In the sum, the total of the arguments, with n_j replaced by $n_j - 1$, is $N - 1$, and the weighted sum of the arguments is $T - j$. It follows that $E(n_j) = NC(N - 1, T - j)/C(N, T)$. By a similar method it follows that, if $\sum a_i = A$, and $\sum i a_i = B$, then the general factorial moment is

$$E\left[\frac{\prod (n_i\ !)}{\prod (n_i - a_i)!}\right] = \frac{N!}{(N - A)!} \frac{C(N - A, T - B)}{C(N, T)}.$$

Thus in principle the joint factorial moments of the n_i can be determined provided we can regard the $C(N, T)$ as known. Some discussion of the asymptotic representation of $C(N, T)$ is given in Section X, but more needs to be known about these coefficients in general.

For the test of departure from expected frequencies we have

$$X^2 = \sum \frac{n_i^2}{\lambda^* \mu^{*i}} - N.$$

Now λ^* and μ^* are functions of N and T only, so are fixed for the conditional distribution. Hence X^2 may be simply regarded as a weighted sum of squares of the n_i. In particular, since

$$E(n_i^2) = \frac{N(N - 1)C(N - 2, T - 2i) + NC(N - 1, T - i)}{C(N, T)}$$

we have

$$E(X^2) = \frac{N}{\lambda^* C(N, T)} \cdot \sum \frac{(N - 1)C(N - 2, T - 2i) + C(N - 1, T - i)}{\mu^{*i}} - N;$$

higher moments may be found similarly.

IX. TEST FOR TREND IN FREQUENCIES

Of particular importance is the test for the reality of any apparent trend in the frequencies—that is, whether the estimated value of μ differs significantly from unity. When N is large, the test may be

made by comparing the difference $1 - \mu^*$ with its standard error, or, what is equivalent, testing $\frac{1}{2}(k-1)N - T$ against its standard error.

When $\mu = 1$, the variance of μ^* reduces to $12/(k^2-1)N$, so that the test statistic, distributed approximately as χ^2 with 1 degree of freedom, is

$$(k^2-1)N(1-\mu^*)^2/12. \tag{13}$$

More directly, the variance of T is

$$[(k^2-1)N]/12,$$

so that an alternative test statistic is

$$12(\tfrac{1}{2}(k-1)N - T)^2/(k^2-1)N. \tag{14}$$

The statistics (13) and (14) are equivalent in large samples since, when μ^* is near to unity, we have

$$\mu^* = 1 - \frac{12(\frac{1}{2}(k-1)N - T)}{(k^2-1)N} + O(N^{-1}),$$

as can be seen from (9).

The exact significance probability is given by the probability of a value of T less than or equal to that observed, which is easily computed directly when N is not large. This probability should be doubled, since both tails of the distribution are relevant to this test. With $\mu = 1$, this probability is simply

$$\sum_{r=0}^{T} C(N, r)/k^N = S(N, T)/k^N.$$

Now the generating function of $S(N, T)$ is

$$[\phi_0(\mu)]^N/(1-\mu) = (1-\mu^k)^N/(1-\mu)^{N+1}.$$

From this representation we readily deduce that

$$S(N,T) = \binom{N+T}{N} - \binom{N}{1}\binom{N+T-k}{N} + \binom{N}{2}\binom{N+T-2k}{N} - \cdots \tag{15}$$

which provides the most convenient means of computation of isolated values of the sum. On putting $T = (k-1)N$ in (15) we have the interesting corollary

$$\binom{kN}{N} - \binom{N}{1}\binom{k(N-1)}{N} + \binom{N}{2}\binom{k(N-2)}{N} - \cdots = k^N.$$

Values of T less than $\frac{1}{2}(k-1)N$ required for significance at the 5 and 1 percent levels of probability have been determined for various values of k and N, and are presented in Table 3. For values of N beyond the range of the Table, the large-sample χ^2-test may be used.

TABLE 3

EXACT TEST FOR EXISTENCE OF TREND
(I.E. OF NULL HYPOTHESIS $\mu = 1$)

5 PERCENT POINT OF T [OR $(k-1)N - T$]

	k		
N	3	4	5
5	1	2	3
6	1	3	4
7	2	4	6
8	3	5	7
9	3	6	9
10	4	7	10
11	5	8	12
12	6	9	13
13	6	11	15
14	7	12	17
15	8	13	18

1 PERCENT POINT OF T [OR $(k-1)N - T$]

	k		
N	3	4	5
5	0	0	1
6	0	1	2
7	1	2	4
8	1	3	5
9	2	4	6
10	3	5	8
11	3	6	9
12	4	7	11
13	5	8	12
14	5	9	14
15	6	11	15

X. EVALUATION OF TAIL PROBABILITIES

When N is large, the calculation of the probabilities of the tails of the distribution is troublesome. Blackwell and Hodges [1959] have given a method for expeditiously finding approximate tail probabilities. The method depends on a transformation of the distribution to a new distribution for which probabilities in the neighbourhood of the mean are to be determined. Daniels [1954] has given equivalent results, expressed explicitly for continuous probability densities, and Good [1957] has given similar results to the term of order N^{-2} of the leading term.

We briefly outline Blackwell and Hodges' results applied to the present distribution. We make use of the fact that the distribution of T is the N-fold convolution of the distribution of X as defined in Section IV.

The moment-generating function of $X - a$, where a is any constant, is $M(s) = E[e^{s(X-a)}]$.

Let s^* be the unique value of s that minimizes $M(s)$, and denote the minimum of $M(s)$ by $m(a)$; note that s^* is a function of a. Then we transform to a new variable Y, for which

$$P(Y = x) = \frac{P(X = x)e^{s^*(x-a)}}{m(a)}. \tag{16}$$

It is readily seen that Y has in fact a probability density with the same range as X. Also, by differentiating the numerator of (16) with respect to s^* and summing, we find that $E(Y) = a$.

Before continuing with Blackwell and Hodges' method, we establish the interesting result that, for any distribution for which the sum of the values of X is a sufficient statistic for the parameter μ, the new variate Y has a distribution of the same form, but with parameter μ^*, the maximum likelihood estimate corresponding to the value $X = a$. This result is probably well known, though we have never seen it discussed. Thus we see that, for distributions of this commonly occurring class, the solution of the maximum likelihood equation is important not only for providing a point estimate, but also for evaluating the tail probabilities corresponding to the particular observed value.

If the sum of the values of X is sufficient for μ, the density of X may be written as

$$h(X)e^{X\theta(\mu)}/f(\mu), \tag{17}$$

where

$$f(\mu) = \sum_x h(x)e^{x\theta(\mu)}.$$

Then

$$M(s) = \sum_x h(x)e^{s(x-a)+xg(\mu)}/f(\mu),$$

so that, for any value of s whatever, a transformed density is given by

$$h(X)e^{X[s+g(\mu)]}/e^{as}M(s).$$

This density is clearly of the same form as that of X.

Now the maximum likelihood equation, corresponding to an observed value a, turns out to be

$$a - \sum_x xh(x)e^{xg(\mu)} / \sum_x h(x)e^{xg(\mu)} = 0,$$

where we have differentiated (17) with respect to $g(\mu)$ rather than μ itself. This is in fact $E(X \mid \mu = \mu^*) = a$. Now from (16) we derived that $E(Y) = a$. It follows therefore that the parameter of the distribution of Y is μ^*.

We can also express $m(a)$ in terms of the maximum likelihood estimator. On putting $x = a$ in (16), we see that $m(a) = P(X = a)/P(Y = a)$, or $P(a \mid \mu)/P(a \mid \mu^*)$.

For the particular distribution we have been considering, therefore

$$m(a) = \left(\frac{\mu}{\mu^*}\right)^a \left(\frac{\phi_0^*}{\phi_0}\right),$$

where we indicate by an asterisk a function of μ^*.

Blackwell and Hodges, by means of the transformation (16), and taking $Na = T$, show that

$$P(X_1 + X_2 + \cdots + X_N = T) = [m(a)]^N P(Y_1 + Y_2 + \cdots + Y_N = T),$$

and thence, that each side is equal to

$$\frac{[m(a)]^N}{\sqrt{2\pi N \kappa_2^*}} \left[1 + \frac{1}{8N}\left(\frac{\kappa_4^*}{\kappa_2^{*2}} - \frac{5}{3}\frac{\kappa_3^{*2}}{\kappa_2^{*2}}\right) + O(N^{-2})\right],$$

or

$$\left(\frac{\mu}{\mu^*}\right)^T \left(\frac{\phi_0^*}{\phi_0}\right)^N \frac{1}{\sqrt{2\pi N \kappa_2^*}} \left[1 + \frac{1}{8N}\left(\frac{\kappa_4^*}{\kappa_2^{*2}} - \frac{5}{3}\frac{\kappa_3^{*2}}{\kappa_2^{*3}}\right) + O(N^{-2})\right] \qquad (18)$$

where the κ_r^* are the cumulants of the distribution of Y; that is, functions of μ^*. The explicit terms in (18) give a satisfactory approximation to $P(T \mid N)$, provided N is large.

We note that the series in (18) depends only on μ^* (i.e., on T), and not on μ. Thus what we have obtained is an asymptotic expansion of $C(N, T)$. In fact,

$$C(N, T) = \frac{\phi_0^{*N}}{\mu^{*T}\sqrt{2\pi N \kappa_2^*}}\left[1 + \frac{1}{8N}\left(\frac{\kappa_4^*}{\kappa_2^{*2}} - \frac{5}{3}\frac{\kappa_3^{*2}}{\kappa_2^{*3}}\right) + O(N^{-2})\right].$$

Thus, $C(N, T)$ may be estimated by substituting the actual values of the cumulants, from the formulae given in Section IV.

As a check on the asymptotic formula, we estimate $C(N, T)$ for the values $k = 4$, $N = 15$, $T = 11$. We deduce $\mu^* = \frac{1}{2}$, $\phi_0 = 15/8$,

$$\kappa_2^* = 194/15^2 = 0.862222,$$

$$\kappa_3^* = 2842/15^3 = 0.842074,$$

$$\kappa_4^* = 1434/15^4 = 0.028326.$$

Hence

$$C(15, 11) \sim \sqrt{\frac{15}{2\pi \cdot 194}}\,\frac{(15/8)^{15}}{(\frac{1}{2})^{11}}\left(1 - \frac{1.805604}{120}\right) = 2{,}784{,}963.$$

The true value is

$$\binom{25}{15} - \binom{15}{1}\binom{21}{15} + \binom{15}{2}\binom{17}{15} = 2{,}784{,}600,$$

from which the estimate by the asymptotic formula is in error by 130 per million.

For significance testing, the cumulative tail probabilities are more important than the individual terms. These cumulative probabilities are also given by Blackwell and Hodges. They give

$$P(T \geq t) = \frac{[m(a)]^N}{\sqrt{2\pi N \kappa_2^*(1-z)}}\left[1 + \frac{1}{8N}\left(\frac{\kappa_4^*}{\kappa_2^{*2}} - \frac{5}{3}\frac{\kappa_3^{*2}}{\kappa_2^{*3}}\right) - \frac{z}{2N}\left(\frac{\kappa_3^*(1-z) + \kappa_3^*(1+z)}{\kappa_2^{*2}(1-z)^2}\right) + O(N^{-2})\right]$$

$$= \frac{P(T = t)}{(1-z)}\left[1 - \frac{z}{2N}\frac{\kappa_3^*(1-z) + \kappa_2^*(1+z)}{\kappa_2^{*2}(1-z)^2} + O(N^{-2})\right]$$

where, for the distribution considered here, $z = \mu/\mu^*$. We note that, as is to be expected, the bracketed series in the cumulative probability depends on μ. The approximation is valid only for $\mu^* > \mu$, and is most effective when z is small—that is, when μ^* is large and the extreme tails of the distribution are being considered.

When we are determining the probability in the lower tail of the distribution, that is $P(T \leq t)$, so that $T < \frac{1}{2}(k-1)N$, and $\mu^* < \mu$, we simply replace z by z^{-1} throughout the formula, and change the sign of κ_3^*.

As a test of the adequacy of this approximation, we apply it to the example for which the individual term was calculated above, namely $k = 4$, $N = 15$, $T = 11$.

Inserting the values found above, we have $z = 2\mu$,

$$P(T \leq 11) = \frac{P(T = 11)}{\left(1 - \frac{1}{2\mu}\right)} \cdot \left[1 - \frac{1}{60\mu}\left\{\frac{\frac{-2842}{15^3}\left(1 - \frac{1}{2\mu}\right) + \frac{194}{15^2}\left(1 + \frac{1}{2\mu}\right)}{\frac{194^2}{15^4}\left(1 - \frac{1}{2\mu}\right)^2}\right\} + O(N^{-2})\right].$$

We consider the adequacy of the approximation when $\mu = 1$, for which we can readily determine the exact probability. We have

$$P(T = 11) = 2{,}784{,}600/4^{15},$$

so the leading term in the approximate probability is

$$2P(T = 11) = 5{,}569{,}200/4^{15} = 0.005187.$$

For the first adjustment we find the factor $1 - 0.078223$ giving $5{,}133{,}560/4^{15} = 0.004781$. The exact value of the denominator is

$$S(15, 11) = \binom{26}{15} - \binom{15}{1}\binom{22}{15} + \binom{15}{2}\binom{18}{15} = 5{,}253{,}680,$$

giving the exact probability 0.004893.

We see that the first adjustment gives an approximation adequate for the purpose of assessing the significance probability. Since both tails of the distribution are relevant to any test of significance, the significance probability is 0.009786; $T = 11$ is thus the 1 percent point of the distribution.

By determining the tail probabilities corresponding to any given value of μ we can in principle set a confidence range for μ — the set of all μ which are not discordant with the observed values N and T.

XI. APPLICATION TO EXPERIMENTAL DATA

The data in Table 4 show numbers in each of the first three instars of immature cowpea aphids (*A. craccivora*), from samples drawn on six different occasions from the same population. Since the experimental conditions were uniform, and the average duration of each instar is the same (about 42 hours at 20°C), the expected numbers are in geometric progression. The Table also gives an overall estimate of the common ratio, 0.529820. In order to determine the growth-rate of the population,

TABLE 4

AGE-DISTRIBUTION OF IMMATURE COWPEA APHIDS (*A. craccivora*)

Sample	Instar I	Instar II	Instar III	N	T	λ^*	μ^*	X^2
1	181	92	51	324	194	179.730	0.526015	0.11
2	148	78	42	268	162	147.737	0.531518	0.01
3	130	54	43	227	140	123.456	0.543412	4.07
4	70	37	21	128	79	69.580	0.543848	0.03
5	88	41	20	149	81	87.710	0.474049	0.13
6	85	42	28	155	98	82.857	0.558629	0.63
Total	702	344	205	1251	754	690.958	0.529820	2.14

we equate this ratio to $e^{-c\rho}$, c being the average duration of instar and ρ the growth-rate.

We then find

$$c\rho = -\log (0.529820) = 0.6352$$

so that

$$\rho = 0.6352/42 \text{ per hour} = 0.01512 \text{ per hour} = 0.363 \text{ per day}.$$

The population grows at the rate of $100(e^{0.363} - 1) = 44$ percent per day.

Table 4 also gives estimates of λ and μ for each sample, and X^2 with 1 degree of freedom measuring departure from the common ratio. Only the largest X^2-value, for sample 3, attains the 5 percent level of significance, so that there is no evidence for departure from hypothesis.

The variance of the estimate of μ from a sample of N is $\mu^2/V(T)$ which reduces when $k = 3$ to

$$\frac{\mu(1 + \mu + \mu^2)^2}{N(1 + 4\mu + \mu^2)}.$$

Using the overall estimate $\mu_0^* = 0.529820$ we find the variance of estimate to be

$$V(\mu^* \mid N) = 0.510813/N.$$

The consistency of the estimates of μ from the different samples may be tested by X^2.

For consistency,

$$X^2 = (0.526015^2 \times 324 + 0.531518^2 \times 268 + \cdots - 0.529820^2 \times 1251)/0.510813$$

$$= 1.84, \text{ with 5 degrees of freedom.}$$

The individual ratios differ no more than would be expected by chance.

After the manner of Section IX, formulae (13) and (14), an alternative statistic for testing consistency is based on comparison of the ratios T/N.

$$V(T/N) = \mu(1 + 4\mu + \mu^2)/N(1 + \mu + \mu^2)^2 = 0.549534/N$$

Hence

$$X^2 = (194^2/324 + 162^2/268 + \cdots - 754^2/1251)/0.549534$$
$$= 1.33.$$

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COMPUTING PROCEDURES FOR ESTIMATING COMPONENTS OF VARIANCE IN THE TWO-WAY CLASSIFICATION, MIXED MODEL[1]

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INTRODUCTION

Methods for estimating variance components from unbalanced data are given in Henderson [1953] for both the random model and the mixed model. The calculations involved in the latter case are somewhat tedious and usually not computationally feasible for data having many classes. This paper outlines the analysis for unbalanced data from a two-way classification with one classification considered fixed. Simplified computing procedures are presented suitable for a large number of levels in the random classification and a reasonable number of levels of the fixed classification.

MODELS AND ESTIMATION

The model for the two-way classification can be taken as

$$x_{ijk} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + e_{ijk} , \qquad (1)$$

where x_{ijk} is the observation and μ is the general mean. α_i is the effect due to the i'th level of the α-class, β_j the effect due to the j'th level of the β-class, $\alpha\beta_{ij}$ the interaction and e_{ijk} a random error term. We will suppose that the number of α-classes in the data is a, the number of β-classes is b, that there are n_{ij} observations in the ij'th subclass, and that s sub-classes have observations in them. All terms except μ are taken as independent random variables in the random model with zero means and variances σ_α^2 , σ_β^2 , $\sigma_{\alpha\beta}^2$ and σ_e^2 respectively. The β-classification will be considered fixed in the mixed model, the variances involved being σ_α^2 , $\sigma_{\alpha\beta}^2$, and σ_e^2 , the interaction terms being random for the particular set of fixed effects occurring in the data. In this case we are assuming an underlying multivariate distribution with x_{ijk} having mean

[1]Parts of this paper are based on the thesis submitted by the first author in partial fulfillment of the requirements of the Ph. D. degree.

value $\mu + \beta_i$ and variance $\sigma_\alpha^2 + \sigma_{\alpha\beta}^2 + \sigma_e^2$: the covariance between x_{ijk} and $x_{ijk'}$ for $k \neq k'$ is $\sigma_\alpha^2 + \sigma_{\alpha\beta}^2$ and that between x_{ijk} and $x_{ij'k'}$ for $j \neq j$ and $k \neq k'$, is σ_α^2 .

Variance components can be estimated in both models by equating linear functions of sums of squares to their expected values, the sums of squares used being reductions in the total sum of squares due to fitting various elements of the model as if it were a fixed model. For example, fitting $(\mu + \alpha_i)$ results in matrix equations of the form

$$\mathbf{P}\hat{\boldsymbol{\alpha}} = \mathbf{y},$$

where $\mathbf{y}$ is the vector of α-class totals $x_{i..}$, and $\hat{\boldsymbol{\alpha}}$ is the vector of estimates of the α's. $\mathbf{P}$ is non-singular, a diagonal matrix of order a, of terms $n_{i.}$. Thus

$$\hat{\boldsymbol{\alpha}} = \mathbf{P}^{-1}\mathbf{y},$$

and the reduction in the total sum of squares due to fitting the α's is

$$R(\mu, \alpha) = \hat{\boldsymbol{\alpha}}\mathbf{y} = \mathbf{y}'\mathbf{P}^{-1}\mathbf{y}.$$

This is the usual uncorrected sum of squares, namely

$$R(\mu, \alpha) = \sum_i x_{i..}^2/n_{i.} \ . \tag{2}$$

Similarly

$$R(\mu, \beta) = \sum_j x_{.j.}^2/n_{.j} \ , \tag{3}$$

$$R(\mu, \alpha, \beta, \alpha\beta) = \sum_i \sum_j x_{ij.}^2/n_{ij} \ , \tag{4}$$

$$R(\mu) = x_{...}^2/n_{..} \ , \tag{5}$$

and

$$R(0) = \sum_i \sum_j \sum_k x_{ijk}^2 \ . \tag{6}$$

The variance components of the random model are estimated by equating the expected values to the observed values of differences among the above uncorrected sums of squares, namely (2)–(5), (3)–(5), (4)–(2)–(3) + (5) and (6)–(4). These cannot be used in the mixed model because, apart from (6)–(4), their expectations then contain functions of the fixed effects. The within-subclasses sum of squares, (6)–(4), can still be used to estimate the error variance as in the random model, and σ_α^2 and $\sigma_{\alpha\beta}^2$ can be estimated from the differences:

$$R(\mu, \alpha, \beta) - R(\mu, \beta),$$

and

$$R(\mu, \alpha, \beta, \alpha\beta) - R(\mu, \alpha, \beta),$$

whose expectations are free of terms in the fixed effects. $R(\mu, \alpha, \beta)$ is the reduction in the total sum of squares due to fitting α and β alone without the interaction terms. This reduction in sum of squares does not occur in the random model analysis and, when required for the mixed model analysis it usually involves a considerable amount of computing. Its relationship to the random model analysis will now be shown and a simplified computing procedure derived.

SIMPLIFIED EXPRESSION FOR R (μ, α, β)

Henderson *et al.* [1959] have shown that fixed effects in a mixed model can be estimated by treating the random effects as fixed and maximizing the joint distribution function of the observations and the random effects. The resulting equations for the two-way classification without interaction are

$$\begin{bmatrix} \mathbf{P} & \mathbf{Q} \\ \mathbf{Q}' & \mathbf{R} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{a}} \\ \hat{\boldsymbol{\beta}} \end{bmatrix} = \begin{bmatrix} \mathbf{y} \\ \mathbf{z} \end{bmatrix} \tag{7}$$

where P is a diagonal matrix, of order a, with terms $n_{i.}$, $\mathbf{R}$ is a diagonal matrix of order $b - 1$ with terms $n_{.j}$, $j \neq b$, $\mathbf{Q}$ is a matrix of order a by $b - 1$ with terms n_{ij}, $j \neq b$, $\mathbf{y}$ is a vector of the $x_{i..}$ totals and $\mathbf{z}$ is a vector of the $x_{.j.}$ totals. $\mathbf{R}$, $\mathbf{Q}$ and $\mathbf{z}'$ have $b - 1$ columns because of omitting the equation for the last β, appropriate to imposing the constraint $\hat{\beta}_b = 0$ in order to have a unique solution. $R(\mu, \alpha, \beta)$ from these equations is

$$\begin{aligned} R(\mu, \alpha, \beta) &= (\hat{\mathbf{a}}'\hat{\boldsymbol{\beta}}') \begin{bmatrix} \mathbf{y} \\ \mathbf{z} \end{bmatrix}, \\ &= (\mathbf{y}'\mathbf{z}') \begin{bmatrix} \mathbf{P} & \mathbf{Q} \\ \mathbf{Q}' & \mathbf{R} \end{bmatrix}^{-1} \begin{bmatrix} \mathbf{y} \\ \mathbf{z} \end{bmatrix}. \end{aligned} \tag{8}$$

This expression for obtaining $R(\mu, \alpha, \beta)$ requires inverting a matrix of order $(a + b - 1)$, which is not feasible in many situations because a, the number of random classes in the data, is large. For example, the analysis of dairy production records in Searle and Henderson [1960] involved 688 herds (random) and 4 age groupings (fixed) so that a matrix of order 691 would need to be inverted for equation (8). However, because of its special form, it can be reduced to inverting a 3×3 matrix. Thus in the general case for the two-way classification the inversion of an $(a + b - 1)$ matrix can be reduced to inverting one of order $(b - 1)$ and this is a considerable reduction in the computing required especially when a, the number of random effects, is large, as is frequently the case.

The simplification of (8) proceeds as follows. Let

$$\begin{bmatrix} \mathbf{P} & \mathbf{Q} \\ \mathbf{Q}' & \mathbf{R} \end{bmatrix}^{-1} = \begin{bmatrix} \mathbf{A} & \mathbf{B} \\ \mathbf{B}' & \mathbf{D} \end{bmatrix}. \tag{9}$$

Then

$$\begin{aligned} \mathbf{A} &= \mathbf{P}^{-1} + \mathbf{P}^{-1}\mathbf{Q}\mathbf{D}\mathbf{Q}'\mathbf{P}^{-1}, \\ \mathbf{B} &= -\mathbf{P}^{-1}\mathbf{Q}\mathbf{D}, \\ \mathbf{D} &= (\mathbf{R} - \mathbf{Q}'\mathbf{P}^{-1}\mathbf{Q})^{-1}, \end{aligned} \tag{10}$$

$$R(\mu, \alpha, \beta) = (\mathbf{y}'\mathbf{z}') \begin{bmatrix} \mathbf{P}^{-1} + \mathbf{P}^{-1}\mathbf{Q}\mathbf{D}\mathbf{Q}'\mathbf{P}^{-1} & -\mathbf{P}^{-1}\mathbf{Q}\mathbf{D} \\ -\mathbf{D}\mathbf{Q}'\mathbf{P}^{-1} & \mathbf{D} \end{bmatrix} \begin{bmatrix} \mathbf{y} \\ \mathbf{z} \end{bmatrix}$$

$$= \mathbf{y}'\mathbf{P}^{-1}\mathbf{y} + (\mathbf{z}' - \mathbf{y}'\mathbf{P}^{-1}\mathbf{Q})\mathbf{D}(\mathbf{z} - \mathbf{P}^{-1}\mathbf{Q}'\mathbf{y}). \tag{11}$$

The matrix $\mathbf{P}$ is easily inverted, being diagonal, and the only non-diagonal matrix to invert is $\mathbf{D} = (\mathbf{R} - \mathbf{Q}'\mathbf{P}^{-1}\mathbf{Q})^{-1}$ of order $b - 1$.

The first term in the above expression is $R(\mu, \alpha)$, and the second can be derived from equations (7). Eliminating

$$\hat{\boldsymbol{\alpha}} = \mathbf{P}^{-1}(\mathbf{y} - \mathbf{Q}\hat{\boldsymbol{\beta}}),$$

gives

$$\hat{\boldsymbol{\beta}} = \mathbf{D}(\mathbf{z} - \mathbf{Q}'\mathbf{P}^{-1}\mathbf{y}). \tag{12}$$

This is easily computed and can then be used to obtain R_β, the reduction in the sum of squares due to fitting the β's in this no-interaction model, as

$$R_\beta = \hat{\boldsymbol{\beta}}'(\mathbf{z} - \mathbf{Q}'\mathbf{P}^{-1}\mathbf{y}). \tag{13}$$

Thus from (11) $R(\mu, \alpha, \beta)$ can be expressed as

$$R(\mu, \alpha, \beta) = R(\mu, \alpha) + R_\beta, \tag{14}$$

the first term of which is part of the random model analysis and the second term comes from (12) and (13).

EXPECTED VALUES

The expectation of $R(\mu, \alpha, \beta)$ can be found by using (8) and (9) and writing

$$R(\mu, \alpha, \beta) = (\mathbf{y}'\mathbf{z}') \begin{bmatrix} \mathbf{A} & \mathbf{B} \\ \mathbf{B} & \mathbf{D} \end{bmatrix} \begin{bmatrix} \mathbf{y} \\ \mathbf{z} \end{bmatrix},$$

$$= (\mathbf{y}'\mathbf{A}\mathbf{y} + \mathbf{z}'\mathbf{B}\mathbf{y} + \mathbf{y}'\mathbf{B}\mathbf{z} + \mathbf{z}'\mathbf{D}\mathbf{z}),$$

$$= \text{tr}\,(\mathbf{A}\mathbf{y}\mathbf{y}' + 2\mathbf{B}\mathbf{z}\mathbf{y}' + \mathbf{D}\mathbf{z}\mathbf{z}'),$$

where $tr(\mathbf{A})$ is the trace of the matrix **A**, the sum of its diagonal terms. After substituting from (1) for the vectors of totals **y** and **z** and also using (1) in (3), (4) and (6) it can be shown, with a certain amount of algebraic manipulation, that the differences used for estimating the variance components have expected values

$$E[R(\mu, \alpha, \beta) - R(\mu, \beta)] = (n_{..} - k_2)\sigma_\alpha^2 + (k_\beta - k_2)\sigma_{\alpha\beta}^2 + (a-1)\sigma_e^2,$$

$$E[R(\mu, \alpha, \beta, \alpha\beta) - R(\mu, \alpha, \beta)] = (n_{..} - k_\beta)\sigma_{\alpha\beta}^2 + (s - a - b + 1)\sigma_e^2,$$

$$E[R(0) - R(\mu, \alpha, \beta, \alpha\beta)] = (n_{..} - s)\sigma_e^2.$$

The variances are estimated by equating the right-hand sides of these equations to the calculated values of the differences in the square brackets of the left-hand side. The term k_2 is one of the coefficients used in the random model analysis, namely $k_2 = \sum_{i=1}^{b} [\sum_{i=1}^{a} n_{ij}^2]/n_{.j}$. The coefficient k_β comes from the expected value of $R(\mu, \alpha, \beta)$ and can be expressed in the form

$$k_\beta = 2 \operatorname{tr} (\mathbf{AU} + 2\mathbf{BV} + \mathbf{DW}), \tag{15}$$

where **U** is a diagonal matrix of order a with terms $\sum_{j=1}^{b-1} n_{ij}^2$ for $i = 1 \cdots a$, **V** is a matrix of order a by $b - 1$ with terms n_{ij}^2 for $i = 1 \cdots a$, and $j = 1 \cdots b - 1$, and W is a diagonal matrix of order $b - 1$ with terms $\sum_{i=1}^{a} n_{ij}^2$ for $j = 1 \cdots b - 1$.

COMPUTING R_β AND k_β

R_β is obtained from computing the following terms:

(i) A square matrix **C**, of order $(b - 1)$ with terms

$$c_{jj} = n_{.j} - \sum_i n_{ij}^2/n_{i.}, \qquad j = 1, \cdots, b-1,$$

and

$$c_{jj'} = -\sum_i n_{ij}n_{ij'}/n_{i.}, \qquad j \neq j' = 1, \cdots, b-1.$$

Computing c_{bj} provides the check that $\sum_{j'=1}^{b-1} c_{jj'} = 0$, for all j, i.e. row and column totals of the augmented **C** are zero.

(ii) A column vector **r**, of order $b - 1$, whose terms are

$$r_j = x_{.j.} - \sum_i n_{ij}\bar{x}_{i..}, \qquad j = 1, \cdots, b-1.$$

Computing r_b provides the check that the sum of all the r_j's is zero

(iii) A column vector, of order $b - 1$, of the estimates of the β's,

$$\hat{\boldsymbol{\beta}} = \mathbf{C}^{-1}\mathbf{r}.$$

(iv) The "inner product" of the terms in the preceding two vectors is R_β:

$$R_\beta = \hat{\boldsymbol{\beta}}'\mathbf{r} = \sum_{i=1}^{b-1} \hat{\beta}_i r_i = \mathbf{r}'\mathbf{c}\mathbf{r}.$$

This is equation (13), the $\mathbf{C}^{-1}$ used here being identical to $\mathbf{D}$.

Expression (15) for k_β is obtained using the elements of $\mathbf{C}^{-1}$, which we shall call $d_{ii'}$, obtained in the calculating of R_β above. The special forms of the matrices involved in (15) enables k_β to be written as

$$k_\beta = \sum_{i=1}^{a} \lambda_i + \sum_{j=1}^{b-1} d_{jj}\left(\sum_{i=1}^{a} f_{i.jj}\right) + 2\sum_{j'\neq j=1}^{b-1}\sum^{b-1} d_{jj'}\left(\sum_{i=1}^{a} f_{i.jj'}\right),$$

where

$$\lambda_i = \sum_{j=1}^{b-1} n_{ij}^2/n_{i.} ,$$

$$f_{i.jj} = (n_{ij}^2/n_{i.})\,(\lambda_i + n_{i.} - 2n_{ij}),$$

and

$$f_{i.jj'} = (n_{ij}n_{ij'}/n_{i.})\,(\lambda_i - n_{ij} - n_{ij'}).$$

The f's, of which $\frac{1}{2}b(b-1)$ in number are required, can be calculated for each i and summed, and the expression is well-suited to evaluation on a computer. Desk calculation can be arranged from the same formula when b is small, and the number of α-classes (random) is not too large. Calculating all of the $\frac{1}{2}b(b+1)$ f's enables the following check to be placed on them:

$$\sum_{j'=1}^{b}\left(\sum_{i} f_{i.jj'}\right) = -\sum_{i} n_{ij}^2 n_{ij}/n_{i.} . \tag{16}$$

The f-values and $\sum_i \lambda_i$ can be obtained simultaneously with the terms of $\mathbf{C}$ and $\mathbf{r}$; R_β is calculated as $\mathbf{r}'\mathbf{C}^{-1}\mathbf{r}$ and k_β is obtained using the elements of $\mathbf{C}^{-1}$ as above.

EXAMPLE

The calculation of R_β and k_β is demonstrated for the small hypothetical example shown in Table 1.

The steps for obtaining R_β are as follows:

(i) The c-values are

$$c_{11} = 53 - 1^2/10 - 3^2/20 - 12^2/40 - 12^2/50 - 25^2/50 = 33.47,$$

$$c_{22} = 45 - 2^2/10 - 6^2/20 \qquad\quad - 12^2/50 - 25^2/50 = 27.42,$$

TABLE 1

HYPOTHETICAL EXAMPLE

i	Number of observations n_{ij}					Mean observed values, $\hat{x}_{i..}$
	j				Totals $n_{i.}$	
	1	2	3	4		
1	1	2	3	4	10	200
2	3	6	4	7	20	300
3	12	—	12	16	40	400
4	12	12	13	13	50	500
5	25	25	—	—	50	600
Totals $n_{.j}$	53	45	32	40	$n_{..} = 170$	
Totals of observed values, $x_{.j.}$	23000	23000	14000	19000		

$$c_{33} = 32 - 3^2/10 - 4^2/20 - 12^2/40 - 13^2/50 = 23.32,$$

$$c_{44} = 40 - 4^2/10 - 7^2/20 - 16^2/40 - 13^2/50 = 26.17,$$

$$c_{12} = -1(2)/10 - 3(6)/20 - 12(12)/50 - 25(25)/50 = -16.48,$$

$$c_{13} = -1(3)/10 - 3(4)/20 - 12(12)/40 - 12(13)/50 = -7.62,$$

and similarly

$$c_{14} = -9.37, \quad c_{24} = -6.02,$$

$$c_{23} = -4.92, \quad c_{34} = -10.78.$$

The check on these values, namely $\sum_{i'=1}^{5} c_{ii'} = 0$, can be seen to hold true; for example

$$c_{11} + c_{12} + c_{13} + c_{14} = 33.47 - 16.48 - 7.62 - 9.37 = 0.$$

(ii) The r-values are obtained using the totals of the observations for the levels of the fixed effects and the means for the levels of the random effects:

$$r_1 = 23000 - 1(200) - 3(300) - 12(400) - 12(500) - 25(600) = -3900,$$

$$r_2 = 23000 - 2(200) - 6(300) - 12(500) - 25(600) = -200,$$

$$r_3 = 14000 - 3(200) - 4(300) - 12(400) - 13(500) = 900,$$

$$r_4 = 19000 - 4(200) - 7(300) - 16(400) - 13(500) = 3200.$$

A check on these is that their sum is zero.

(iii)

$$\mathbf{C}^{-1} = \mathbf{D} = \begin{bmatrix} 33.47 & -16.48 & -7.62 \\ -16.48 & 27.42 & -4.92 \\ -7.62 & -4.92 & 23.32 \end{bmatrix}^{-1}$$

(iv)

$$R_\beta = \mathbf{r}'\mathbf{D}\mathbf{r}$$

$$= (-3900, -200, 900) \begin{bmatrix} .053824 & .036902 & .025373 \\ .036902 & .063205 & .025393 \\ .025373 & .025393 & .056530 \end{bmatrix} \begin{bmatrix} -3900 \\ -200 \\ 900 \end{bmatrix}$$

$$= 736703.$$

Calculating k_β involves the elements of $\mathbf{D}$ and the f-values. The latter, together with the λ_i-terms are shown in Table 2. The calculations for $i = 1$ are as follows.

$$\lambda_1 = (1^2 + 2^2 + 3^2)/10 = 1.40,$$

$$f_{1,11} = 1^2(1.4 + 10 - 2)/10 = .94,$$

$$f_{1,22} = 2^2(1.4 + 10 - 4)/10 = 2.96,$$

$$f_{1,33} = 3^2(1.4 + 10 - 6)/10 = 4.86,$$

$$f_{1,12} = 1(2)(1.4 - 1 - 2)/10 = -.32,$$

$$f_{1,13} = 1(3)(1.4 - 1 - 3)/10 = -.78.$$

Similarly $f_{1,14} = -1.44$, $f_{1,23} = -2.16$, $f_{1,24} = -3.68$ and $f_{1,34} = -6.72$. The sums of these terms, over all values of i, are shown in Table 2 from which the f-values can be checked by the expression (16); for example

$$\sum_i (f_{i,11} + f_{i,12} + f_{i,13} + f_{i,14})$$

$$= 505.8357 - 360.9718 - 113.1132 - 158.0607$$

$$= -126.31$$

$$= -4^2(1)/10 + 7^2(3)/20 + 16^2(12)/40 + 13^2(12)/50$$

$$= -(1.60 + 7.35 + 76.80 + 40.56).$$

From the c's and the f's k_β is now computed as

$$k_\beta = 45.79 + [505.8357(.053824) + 436.5532(.063205) + 212.4332(.056530)]$$

TABLE 2

TERMS USED IN CALCULATING k_β

i	λ_i	$f_{i,11}$	$f_{i,22}$	$f_{i,33}$	$f_{i,44}$	
1	1.40	.9400	2.9600	4.8600	5.4400	
2	3.05	7.6725	19.8900	12.0400	22.1725	
3	7.20	83.5200		83.5200	97.2800	
4	9.14	101.2032	101.2032	112.0132	112.0132	
5	25.00	312.5000	312.5000	—	—	
Total	45.79	505.8357	436.5532	212.4332	236.9057	
i	$-f_{i,12}$	$-f_{i,13}$	$-f_{i,14}$	$-f_{i,23}$	$-f_{i,24}$	$-f_{i,34}$
1	.3200	.7800	1.4400	2.1600	3.6800	6.7200
2	5.3550	2.3700	7.2975	8.3400	20.8950	11.1300
3	—	60.4800	99.8400	—	—	99.8400
4	42.7968	49.4832	49.4832	49.4832	49.4832	56.9868
5	312.5000	—	—	—	—	—
Total	360.9718	113.1132	158.0607	59.9832	74.0582	174.6768

$$- 2[360.9718(.036902) + 113.1132(.025373) + 59.9832(.025393)]$$

$$= 77.16.$$

This procedure for obtaining R_β and k_β may not appear greatly more straight-forward than inverting the matrix required in (8) which in this case is the 8×8 matrix

$$\begin{bmatrix}
10 & & & & & 1 & 2 & 3 \\
 & 20 & & & & 3 & 6 & 4 \\
 & & 40 & & & 12 & 0 & 12 \\
 & & & 50 & & 12 & 12 & 13 \\
 & & & & 50 & 25 & 25 & 0 \\
1 & 3 & 12 & 12 & 25 & 53 & & \\
2 & 6 & 0 & 12 & 25 & & 45 & \\
3 & 4 & 12 & 13 & 0 & & & 32
\end{bmatrix}.$$

Advantages are apparent however, when one considers the case of a

large number of levels of the random classification 500 say, instead of 5. The matrix to be inverted would then be of order 503 while the procedure outlined here would still only require inverting a 3×3. The calculation of its terms the c's and of the terms for k_β, the f's, is still lengthy but can be accomplished separately for each i and summation made over i. This can be arranged quite straightforwardly for a desk calculator and is easily organized for an electronic computer such as the IBM 650, for example.

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OPTIMUM SAMPLE SIZE IN ANIMAL DISEASE CONTROL[1]

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1. INTRODUCTION

The objective of an animal disease control program would either be (*a*) to completely eradicate a disease or alternatively (*b*) to reduce the incidence of a disease to a low level and then to keep it in check. In the case of (*b*) the causative organism might not be completely stamped out.

If a disease has not obtained a strong foothold in a country, then objective (*a*) clearly is justified and perhaps the most drastic methods of control are in order. If, on the otherhand, a disease is widely distributed both geographically and zoologically, then alternative (*b*) might be more realistic. This implies that the objective of a particular control program should take into account the cost of the program relative to the price of the consequence if there were no control.

A case in point is the method of control for Pullorum disease (Salmonella pullorum) in poultry. The active form of the disease causes an enteritis in baby chicks which may result in high death losses. Chicks which recover may be carriers of the disease as adults. Female carriers may then transmit the organism via the egg to their progeny, where the disease again may become epidemic. Other species of domestic birds, and numerous wild species including pheasants, quail, and even foxes, cats, swine, cattle and man, have been reported as potential carriers of Pullorum.

Control of this disease is based on a blood testing technique. Samples of blood, collected from each member of an adult flock, are tested against an antigen of pullorum organisms for agglutinizing antibodies. Positive reactors to the blood test are judged to be disease carriers and therefore are removed from the flock and slaughtered.

The blood agglutination test, carried out in most states for the past three or four decades, has now reduced the disease to one of relatively

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minor importance. For example, the number of reactors reported by participants in the Iowa Control program was less than .07 of one percent in 1959 while in the Massachusetts program no positive reactors were reported in that year.

When a disease such as Pullorum is widely distributed but at a low incidence on a state-wide or national level, it becomes problematical whether to continue past practices of completely blood testing all birds in a flock, or whether blood testing only a sample, or even no birds at all, of each flock might be more economical.

The present paper investigates the extent to which 100 percent blood testing is justified, assuming random, that is binomial, infestation of adult flocks. Specifically, we attempt to determine the most economical flock proportion to be blood tested in any given year and locale, as a function of certain values and costs and of the prevailing binomial infestation rate.

Economic optimizations in the presence of binomial a priori distributions have been studied previously, as for example in [1], [2], [3] and [4]. However, this prior work is almost entirely concerned with industrial inspection problems. The present paper is intended in part to illustrate the fact that such methodology, initially intended for industrial application, is equally applicable in the biological realm.

We recognize that the assumption of binomial infestation might in certain instances be improved upon, by suitable contagion models for example. However, this assumption seems not unreasonable in the case of Pullorum; in this case, the adult flock is composed of birds which, though able to transmit the disease to their progeny through the egg, have low contagious influence as carriers.

2. ALTERNATIVE FLOCK TESTING POLICIES; VALUES AND COSTS

We consider the following one-parameter (the parameter is n) family of flock testing policies:

> Sample and blood test n birds out of a flock of N. If the sample contains no reactors (reaction assumed equivalent to infection), return the n birds to the flock and blood test no more. If the sample contains one or more reactors, blood test the entire flock; slaughter all discovered reactors.

The relative economic worth of each of these $N + 1$ competing flock testing policies are now evaluated in the light of the following values and costs.

i: blood test cost per bird,
c: carcass value per bird,
$a(k)$: average value of a member of a flock of size N that contains k undiscovered reactors,
$b(k)$: value of a non-reactor from a completely tested flock of size N containing k discovered reactors.

Note that $a(0) = b(0)$ is the value of a member of a flock containing no reactors. Again, the value of a discovered reactor from a completely tested flock is c. Finally, the precise shapes of the function $a(k)$ will depend on the likelihood that the progeny from a mating involving an undiscovered reactor will become acutely infected, thereby precipitating an epidemic in the progeny flock. The shape of the function $b(k)$ will relate largely to loss of good-will. If good-will is not an important factor, it will not be unreasonable to set $b(k) = b(0)$ for all k; indeed, this is the assumption made at the end of Section 5.

3. PRELIMINARY CONSIDERATIONS

Computationally tractable forms of $a(k)$ and $b(k)$ are as follows.

$$\begin{aligned} a(0) &= A,\ a(k) = \alpha \quad \text{for} \quad k \neq 0, \\ b(0) &= A,\ b(k) = \beta \quad \text{for} \quad k \neq 0. \end{aligned} \tag{1}$$

It is shown below that the most profitable n is either 0 or N. If this can, for the moment, be assumed, then the derivation of the most profitable sample size (i.e. the choice between 0 and N) becomes a matter of simple arithmetic, at least for the limiting cases of very small or very large flock size N.

Consider a large number M of birds, grouped into m flocks of $N = M/m$ birds. The case of very small flock size is typified by $N = 1$, while the case of very large flock size is typified by $m = 1$.

For $N = 1$, the average value of the M birds (i.e. one-bird flocks) equals

$$M(1 - \pi)A + M\pi\alpha, \qquad \text{if} \quad n = 0, \tag{2a}$$

$$M(1 - \pi)A + M\pi c - Mi, \qquad \text{if} \quad n = N\,(=1), \tag{2b}$$

so that 100 percent testing will be more (less) profitable than no testing according to whether

$$\pi(c - \alpha) > (<)\, i. \tag{3}$$

For $m = 1$, the average value of the M birds (i.e. one flock of M birds) equals

$$M(1 - \pi)\alpha + M\pi\alpha = M\alpha, \qquad \text{if } n = 0, \tag{4a}$$

$$M(1 - \pi)\beta + M\pi c - Mi, \qquad \text{if } n = N\,(=M), \tag{4b}$$

so that 100 percent testing will be more (less) profitable than no testing according to whether

$$\beta - \alpha > (<)\ \pi(\beta - c) + i. \tag{5}$$

Expressions (2*a*) and (2*b*) arise from the fact that, under both zero and complete testing, a proportion $(1 - \pi)$ of the M one-bird flocks will be disease-free, contributing an amount $M(1 - \pi)\ A$ to average value. In addition, there will be a value contribution from the $M\pi$ one-bird flocks containing a reactor; this contribution will amount to $M\pi\alpha$ in the case of no testing and to $M\pi c$ in the case of 100 percent testing. Finally, there is the testing cost Mi that is incurred under 100 percent testing.

Expressions (4a) and (4b) arise from the fact that a very large flock will contain an approximate proportion π of reactors; hence, under 100 percent testing, there will be approximately $M\pi$ birds contributing carcass value c to the flock, and approximately $M(1 - \pi)$ birds contributing value β. Similarly, if M is large enough to make $M\pi$ large, the flock of M birds will contain at least one reactor with probability essentially 1, leading to an average per-bird value of α in the absence of testing.

The criteria represented by (3) and (5) constitute an almost adequate solution for the case of the value assumptions given in (1). The further computations of Section 4 will serve only to validate the assertion that the most profitable sample size must either be zero or N, and will lead, as well, to the analogues of (3) and (5) for flocks of intermediate size.

4. THE COMPUTATION OF THE MOST PROFITABLE SAMPLE SIZE FOR THE CASE OF CONSTANT VALUE DIFFERENCE $b(k) - a(k)$

This is the case typified by form (1) of the functions $a(k)$ and $b(k)$. The computations proceed as follows. Let

$$\phi_k = \text{the binomial probability of } k \text{ reactors in a flock of size } N = \binom{N}{k} \pi^k (1 - \pi)^{N-k}, \tag{6}$$

and let

$$h_{n,k} = \text{the hypergeometric probability of obtaining } n \text{ non-reactors when drawing a random sample of size } n \text{ from a flock of } N \text{ birds containing } k \text{ reactors and}$$

$$(N - k) \text{ non-reactors} = \binom{N-k}{n} \Big/ \binom{N}{n}. \tag{7}$$

Then for any particular one of the $(N + 1)$ alternative policies presented in Section 2, say the policy corresponding to sample size n,

$$\Pr\{\text{number of reactors in the flock} = k; \text{ number of reactors in the sample} = 0\} = \phi_k h_{n,k}, \tag{8}$$

and the "profit" ensuing if the number of reactors in the flock equals k and the number of reactors in the sample equals 0 is

$$Na(k) - ni. \tag{9}$$

Hence the contribution to expected profit of the events involving no reactors in the sample equals the sum of the products of (8) and (9):

$$\sum_{k=0}^{N-n} [Na(k) - ni] \cdot \phi_k \cdot h_{n,k}. \tag{10}$$

Again, for the same sample size n,

$$\Pr\{\text{numbers of reactors in the flock} = k; \text{ number of reactors in the sample} > 0\} = \phi_k \cdot (1 - h_{n,k}), \tag{11}$$

and the "profit" ensuing if the number of reactors in the flock equals k and the number of reactors in the sample exceeds 0 is

$$(N - k) \cdot b(k) + kc - Ni. \tag{12}$$

Hence the contribution to expected profit of the events involving one or more reactors in the sample equals the sum of the products of (11) and (12):

$$\sum_{k=0}^{N} ((N - k) \cdot b(k) + kc - Ni) \cdot \phi_k \cdot (1 - h_{n,k}). \tag{13}$$

Total expected profit will equal the sum of (10) and (13), which, neglecting terms not involving n and using the fact that $h_{n,k} = 0$ for $k \geq N - n + 1$, can be written

$$\sum_{k=0}^{N-n} \{N \cdot [a(k) - b(k)] + k \cdot [b(k) - c] + (N - n) \cdot i\} \cdot \phi_k \cdot h_{n,k}. \tag{14}$$

Expression (14) is further reducible to

$$(1 - \pi)^n \cdot \{N \cdot E[a(k) - b(k)] + E[k \cdot (b(k) - c)] + (N - n) \cdot i\}, \tag{15}$$

where the expectation $E[\ ]$ is with respect to the chance variable k having a binomial distribution with parameters $(N - n)$ and π. This type of expectation arises from the fact that

$$\phi_k h_{n,k} = (1 - \pi)^n \left[\binom{N - n}{k} \pi^k (1 - \pi)^{N-n-k} \right].$$

Further reduction leads, except for the additive term $(1-\pi)^N \cdot N(\beta-\alpha)$, to the expression

$$(1 - \pi)^n (T - nS) \equiv P(n), \tag{16}$$

where

$$T = N[\alpha - \beta + \pi(\beta - c) + i], \tag{17}$$

$$S = \pi(\beta - c) + i > 0. \tag{18}$$

Differencing $P(n)$ now yields

$$\Delta(n) = P(n + 1) - P(n) = (1 - \pi)^n[(n\pi - 1)S - \pi(T - S)],$$

which shows that $\Delta(n)$ is negative for $n < (T/S) + (1/\pi) - 1$, and is positive for $n > (T/S) + (1/\pi) - 1$. This implies that no $P(n)$ for $0 < n < N$ can be larger than the larger of $P(0)$ and $P(N)$, which in turn implies that the most "profitable" sample size n either is 0 or N. Establishing this fact (which is reminiscent of conclusions reached in [1] and [2]) was one of the two objectives set for this section in the last paragraph of Section 3.

The second objective set for this section was to derive a condition analogous to (3) and (5) for determining the relative profitabilities of the two sample sizes 0 and N for intermediate flock size N. But this now is simply a matter of comparing $P(0)$ and $P(N)$, where $P(n)$ is given by (16). This yields the conclusion that 100 percent testing is more (less) profitable than no testing at all according to whether

$$(\beta - \alpha)[1 - (1 - \pi)^N] > (<)\ \pi(\beta - c) + i. \tag{19}$$

We note that (19) does indeed specialize to (3) and (5) for N equal, respectively, to 1 and to ∞.

Although details are outside the scope of this paper, it may be of interest to point out that condition (3) arises naturally in the computation of the sequential Bayes test policy for the value assumptions (1). Consider the much (though no doubt impractically) enlarged set of flock testing policies consisting of all sequential plans with terminal acts A and R:

A : Stop testing; collect c for every reactor culled out so far; return non-reactors to the flock; eventually collect α or β per bird of the unculled portion of the flock, depending on whether or not this portion contains at least one reactor, unless the entire flock is reactor-free, in which case collect A.

R : Test 100 percent; collect c for reactors, and β for non-reactors, unless the entire flock is reactor-free, in which case collect A.

A straightforward application of the methodology given in [2] then shows that 100 percent testing is the most economic of the policies in this enlarged set if $\pi(c - \alpha) > i$. However, the complementary prescription for no testing if $\pi(c - \alpha) < i$ does *not* apply in this case.

5. THE COMPUTATION OF THE MOST PROFITABLE SAMPLE SIZE FOR THE CASE OF LINEARLY INCREASING VALUE DIFFERENCE $b(k) - a(k)$.

A value assumption alternative to (1) is

$$a(k) = A - \frac{k}{N}(A - \gamma), \qquad 0 \leq k \leq N,$$
$$b(k) = A - \frac{k}{N}(A - \delta), \qquad 0 \leq k \leq N. \tag{20}$$

Using (15) [which was derived without reference to any specific form of $a(k)$ and $b(k)$], expected profit now becomes, except for additive constants not involving n,

$$P(n) = (1 - \pi)^n \left(\frac{N - n}{N}\right)(T + nS), \tag{21}$$

where

$$T = (A - \delta)(\pi - \pi^2)(N - 1) + N[\pi(\gamma - c) + i], \tag{22}$$

$$S = (A - \delta)\pi^2 \geq 0. \tag{23}$$

The function $P(n)$ given by (21) is best described in terms of the following five parametric cases.

Case I: $S > 0$, $T \geq 0$. As n increases from $-\infty$, $P(n)$ rise steadily from $-\infty$, crosses the n-axis at $n = -T/S$, equals T at $n = 0$, turns downward somewhere between $n = -T/S$ and $n = N$, crosses the n-axis once more at $n = N$, turns upward somewhere beyond $n = N$, and approaches the n-axis asymptotically from below as n approaches $+\infty$.

Case II: $S > 0$, $0 > T > -NS$. As n increases from $-\infty$, $P(n)$ rises steadily from $-\infty$, equals T at $n = 0$, crosses the n-axis at $n = -T/S$, turns downward somewhere between $n = -T/S$ and $n = N$, crosses the n-axis once more at $n = N$, turns upward somewhere beyond $n = N$, and approaches the n-axis asymptotically from below as n approaches $+\infty$.

Case III: $S > 0$, $T \leq -NS$. As n increases from $-\infty$, $P(n)$ rises

steadily from $-\infty$, equals T at $n = 0$, crosses the n-axis at $n = N$, turns downward somewhere between $n = N$ and $n = -T/S$, crosses the n-axis once more at $n = -T/S$, turns upward somewhere beyond $n = -T/S$, and approaches the n-axis asymptotically from below as n approaches $+\infty$.

Case IV $S = 0$; $T > 0$. As n increases from $-\infty$, $P(n)$ decreases steadily from $+\infty$, equals T at $n = 0$, crosses the n-axis at $n = N$, turns upward somewhere beyond $n = N$, and approaches the n-axis asymptotically from below as n approaches $+\infty$.

Case V: $S = 0$, $T \leq 0$. As n increases from $-\infty$, $P(n)$ increases steadily from $-\infty$, equals T at $n = 0$, crosses the n-axis at $n = N$, turns downward somewhere beyond $n = N$, and approaches the n-axis asymptotically from above as n approaches $+\infty$.

Cases IV and V are easily summarized as follows: If $A = \delta$ (corresponding, as indicated at the end of Section 2, to the absence of the good-will factor), then the only policies in contention are 100 percent testing ($n = N$) and no testing ($n = 0$), and 100 percent testing will be more (less) profitable than no testing according to whether

$$\pi(c - \gamma) > (<)\, i. \tag{24}$$

It seems of interest to note the resemblance of (24) and (3).

Cases III and V are summarized by: If $T + NS \leq 0$, it is most economical to test 100 percent.

For Case II, the most economical sample size is the n between $-T/S$ and N at which $P(n)$ turns downward. This case is of interest since it establishes the possibility of an optimum sample size other than 0 or N. This possibility has already been noted in [3].

For Case I, the most economical sample size is either $n = 0$ or the n at which $P(n)$ turns downward, depending on the relative magnitudes at these two sample sizes. Note that, for $T = 0$, the n at which $P(n)$ turns downward must be greater than zero, so that, as in Case II, the most economical sample size will be other than 0 or N.

6. EXAMPLE AND CONCLUSIONS.

Consider the case when good-will is not a factor, i.e. the case of constant $b(k)$. In this case both the formulation of Section 4 and that of Section 5 imply that only the two policies of zero and 100 percent testing are in contention, the choice between these depending on the direction of a simple inequality.

Defining the *critical testing cost* i_c to be the testing cost for which zero and 100 percent testing are equally economical, it seems of interest to compute i_c for both formulations, using comparable value figures.

A typical value for a non-reactor in a fully tested flock is \$3, a typical average value of a member of an untested flock is \$2.40, and typical values for c, π and N are \$.50, 10^{-5} and 500.

Computing i_c in the spirit of Section 4, we therefore set $A = \beta = \$3$ and $\alpha = \$2.40$. Replacing $1 - (1 - \pi)^N$ by $N\pi$ (allowable since $N\pi$ is small), criterion (19) then becomes $\$3 \times 10^{-3} > (<) \$2.5 \times 10^{-5} + i$, which means that $i_c = \$0.003$, i.e. that no testing is most profitable unless the cost of testing falls below 3 mills per bird.

Computing i_c in the spirit of Section 5, we set $A = \delta = \$3$. In addition, we interpret \$2.40 to be the value of the linear function $a(k)$ evaluated at $k = N\pi$, the expected number of reactors in the flock. This implies a per-bird disaster value of $\gamma = -\$6 \times 10^4$ for an unsuspected 100 percent infected flock. Criterion (24) then becomes $\$0.6 > (<) i$, which means that $i_c = \$0.60$, i.e. that 100 percent testing is most profitable unless the cost of testing rises above 60¢ per bird.

In practice, the cost of testing is approximately seven cents per bird. Since this cost is well bracketed by the critical costs 0.3¢ and 60¢ derived above, we learn that the shape of the value function $a(k)$ [and of course also that of $b(k)$] must be determined rather accurately if the methodology presented here is to be applied.

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NUMERICAL ASPECTS OF THE REGRESSION OF OFFSPRING ON PARENT[1]

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INTRODUCTION

In an earlier paper (Bohren, McKean, and Yamada, [1961]) three currently employed techniques for estimating the regression of offspring on parent, and thereby heritability in the narrow sense, were compared and contrasted with respect to their efficiencies of estimation. The general conclusion, based on theoretical considerations and an empirical study of five generations of a closed poultry flock (Yamada, Bohren, and Crittenden, [1957]), was that under the circumstances considered, the method of regression of offspring means on parent's record (method 1) was inferior to the method of regression of individual offspring on parent (method 2) (with the parent's record repeated once for each of its offspring) and to (method 3) the Kempthorne-Tandon technique (Kempthorne and Tandon, [1953]).

The success of the Kempthorne-Tandon technique depends upon knowledge of a parameter ρ, the correlation between deviations of two offspring of the same parent from the predicted breeding value of the parent, and its expected superiority over the second method depends upon the magnitude of ρ. Usually ρ is guessed in the light of prior knowledge, and weights are assigned to the families according to the guessed value of ρ. In the first paper it was shown that, under the assumption of all genetic variance being additive, $\rho \leq .067$ or $\leq .079$, depending upon whether the mating structure is random or hierarchal.

The results obtained in the previous paper specifically depended upon the particular distribution of family sizes encountered in the five analyses, and upon the accuracy of the estimated values of $T = \rho/(1-\rho)$. The purposes of this paper are to consider the efficiency loss incurred by mis-guessing ρ in the Kempthorne-Tandon technique, and to investigate the factors involved in the relative efficiency of the other two methods.

THEORY

We consider a breeding experiment in which s sires are selected

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from the population, sire i being mated to a random sample of d_i distinct dams. The mating structure is then hierarchal, with the progeny of sire i having phenotypic values given by the model

$$Y_{ijk} = \mu_i + \beta(X_{ij} - \mu) + e'_{ijk}, \tag{1}$$

which is equation (11) of the previous paper.

It has been pointed out that the three methods under consideration are merely special cases of the general unbiased weighted regression estimation procedure. The difference between the methods involves only the weights applied to each progeny-group deviation: (1) $w_{ij} = 1$ for the progeny means on parents technique, (2) $w_{ij} = n_{ij}$ for the repeated parents technique, and (3) $w_{ij} = n_{ij}/(1 + n_{ij}\tau)$ for the Kempthorne-Tandon technique, where τ is a guessed value of T. If $\tau = T$, the third technique is the minimum variance technique, whereas, if $\tau = 0$, the third technique reduces to the second. Furthermore, when the family sizes are equal ($n_{i1} = n_{i2} = \cdots$, for all i), all three methods are identical in efficiency. Since most experimental data will involve unequal family sizes, interest will center on considering this situation.

The question, "When may I use method 1 with little loss in efficiency?", is a pertinent one. First, let us examine the optimum choice of weights for which the variance of the estimate of β will be minimized. These optimal weights w_{ij}^* (say), where $w_{ij}^* = n_{ij}/(1 + n_{ij}T)$, will be approximately equal (hence method 1 appropriate), for $T > 0$, under one or more of three distinct sets of circumstances:

1) All n_{ij} are large. This follows immediately from

$$\lim_{n_{ij}\to\infty} \left[\frac{n_{ij}}{1 + n_{ij}T}\right] = \frac{1}{T}.$$

2) S_n^2, the variance of the family sizes, is zero or very small.

3) T is large. This follows from the fact that

$$\lim_{\substack{T\to\infty \\ (\text{or } \rho\to 1)}} \frac{w_{ij}^*}{w_{i'j'}^*} = 1,$$

independent of n_{ij} and $n_{i'j'}$; thus for large T, $w_{ij}^* \doteq w_{i'j'}^*$. In view of this, method 1 may also be considered as a special case of method 3 where τ, the guessed value of T, is allowed to approach ∞.

It is of interest, therefore, to determine a readily accessible statistic which depends upon $\bar{n}$ (the average dam family size), S_n^2, and T, upon which a decision to use or not use method 1 as opposed to method 2 may be based.

It is easy to show that the coefficient of variation among the optimal

weights w_{ij}^* is approximately

$$\psi(T) = \frac{S_n}{\bar{n}(1 + \bar{n}T)} = \frac{C.V.(n)}{1 + \bar{n}T},$$

where $C.V.(n) = S_n/\bar{n}$ = coefficient of variation of the dam family sizes. Since $\psi(T)$ is a function of all three of the statistics mentioned above, it is of interest to consider the relationship between relative efficiency (Min $V(\hat{\beta})/V(\hat{\beta})$) of the various techniques and $\psi(T)$ [even though $\psi(T)$ may seriously differ from the true coefficient of variation of the w_{ij}^*].

For any choice of τ, we may define

$$\psi(\tau) = C.V.(n)/(1 + \bar{n}\tau). \tag{2}$$

Clearly, $\psi(0) = C.V.(n)$, $\psi(\infty) = 0$, and $\psi(\tau)$ is a monotonically decreasing function of τ. Since the range $0 \leq \tau \leq \infty$ corresponds one-to-one to the range in ψ of $C.V.(n) \geq \psi \geq 0$, it is more convenient to express graphically a relationship between ψ, T, and relative efficiency rather than τ, T, and relative efficiency.

Given a fixed set of family sizes $n_{11}, n_{12}, \cdots$ the relative efficiency is a function of T, the true unknown parameter of the population, and τ, the guessed value. Because of the one-to-one relationship between τ and $\psi(\tau)$, the relative efficiency may be expressed as a function of T and ψ. The explicit form of this function may be obtained by solving equation (2) for τ and substituting the resulting expression in ψ into the equation for relative efficiency:

$$R(T, \tau) = \sum_{i=1}^{\dot{s}} (1/\sigma_{\hat{\beta}_i}^2)/\sum_{i=1}^{\dot{s}} (1/\sigma_{\hat{\beta}_i^*}^2),$$

where $\hat{\beta}_i$ = estimated regression within the ith sire using τ as the guessed value of T,

$\hat{\beta}_i^*$ = estimated regression within the ith sire using $\tau = T$ (optimum), and

$$\sigma_{\hat{\beta}_i}^2 = \sigma^2(1 - \rho) \sum_j n_{ij} \frac{1 + n_{ij}T}{(1 + n_{ij}\tau)^2} \frac{(X_{ij} - \bar{X}_{i.})^2}{[\sum_j w_{ij}(X_{ij} - \bar{X}_{i.})^2]^2},$$

$$\sigma_{\hat{\beta}_i^*}^2 = \sigma^2(1 - \rho)/\sum_j w_{ij}^*(X_{ij} - \bar{X}_{i.})^2,$$

which correspond to equations (15) and (16) of the previous paper.

The graph of a typical relationship between ψ, T, and relative efficiency is given in Figure 1. The x- and y-coordinates of any point on the surface pictured represent respectively, the coefficient of varia-

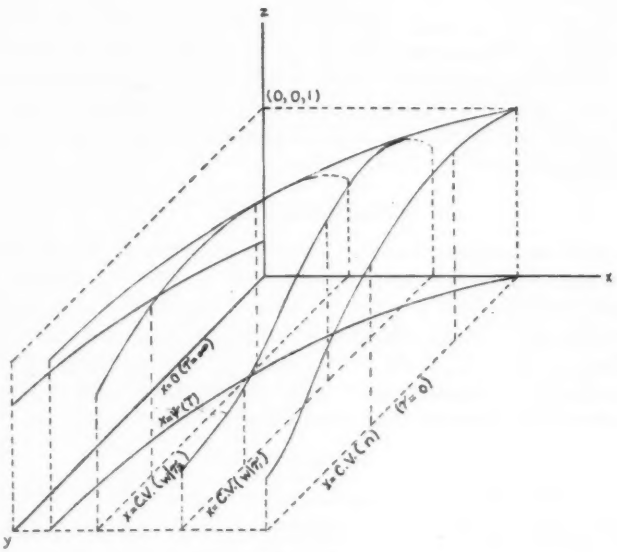

FIGURE 1.

GRAPHICAL REPRESENTATION OF A TYPICAL RELATIONSHIP BETWEEN $x = \psi$, $y = T$, AND z = RELATIVE EFFICIENCY.

tion of the weights resulting from a choice of τ, and the true value of the parameter T, whereas the z-coordinate is the resultant relative efficiency. Several interesting properties should be noted:

1) The points in the (x, y)-plane corresponding to $\tau = T$ (optimal efficiency) lie on a curve whose equation is $x = \psi(T)$. The surface representing relative efficiency thus has a ridge which coincides with the projection of this curve onto the plane $z = 1$.
2) The relative efficiency falls off from this ridge in all directions.
3) The relative efficiency of method $1(\tau = \infty)$ is a strictly increasing function of T.
4) The relative efficiency of method $2(\tau = 0)$ is a strictly decreasing function of T.
5) The relative efficiency of method $3(0 < \tau < \infty)$ is strictly increasing for $0 \leq T < \tau$ and strictly decreasing for $\tau < T < \infty$.
6) For any fixed value T, relative efficiency is a strictly increasing function of τ for $0 \leq \tau < T$ and strictly decreasing for $\tau > T$. This family of curves, generated by all possible T values, expresses graphically the consequences of mis-guessing T.

7) If $C.V.(n)$ is small, the whole picture is condensed along the x-axis so that mis-guessing the value of T will not result in serious loss in efficiency. If $C.V.(n) = 0$, the surface is degenerate, and reduces to the line ($x = 0$, $z = 1$). Alternatively large values of $C.V.(n)$ may result in serious efficiency loss if $| \tau - T |$ is large.

AN ILLUSTRATION

In order to consider the effect of a poor guess for ρ, we will consider the poultry population previously studied by Bohren, McKean and Yamada [1961]. Five years data, 1952–1956 inclusive, are included in the analysis. The information pertinent to the population size and structure are given in Table 1 along with the average family sizes and the coefficients of variation of n. The relative efficiencies of the three methods for the year 1952 are shown in Table 2 for a range of values

TABLE 1

THE FAMILY STRUCTURE OF THE POPULATIONS STUDIED.

Year	No. Sires	No. Dams	No. Pullets	Average Family Size	C.V. (Family Size)
1952	10	106	605	5.7	.74
1953	10	92	877	9.5	.43
1954	11	78	573	7.3	.41
1955	18	108	852	7.9	.47
1956	20	132	715	5.4	.54

of T and τ between zero and .07. This covers most of the theoretical range of ρ, under the assumption of additive genetic variance, as found by Bohren, McKean, and Yamada [1961] and includes the estimates of T obtained from these data. It is seen that in no case is the efficiency of either the repeated parent technique ($\tau = 0$) or the Kempthorne-Tandon technique less than .97. If an intermediate value of τ is chosen under the Kempthorne-Tandon technique (say .03) it is seen that the efficiency does not decline below .99. The efficiency of the means technique is seen to be consistently poorer than the other two techniques.

Analogous tables were generated for the years 1953–1956. Essentially identical results were obtained for all five years analyzed. In all years the relative efficiency of the Kempthorne-Tandon technique remains above 97 percent for $T \leq .07$ and $\tau \leq .07$.

Method 1 was consistently less efficient than method 2 in all years

TABLE 2

RELATIVE EFFICIENCIES OF THE THREE METHODS OF ESTIMATING β RELATIVE TO THE MINIMUM VARIANCE ESTIMATOR OF $\beta(T = \tau)$ FOR VARIOUS SMALL VALUES OF T FOR 1952 DATA.

T	Method 1 (Means Tech.)	Values of τ used in the KT technique (Method 3)							
		.00[2]	.01	.02	.03	.04	.05	.06	.07
.00	.5836	1.0000	.9988	.9958	.9919	.9872	.9822	.9770	.9716
.01	.6083	.9988	1.0000	.9991	.9969	.9938	.9901	.9861	.9818
.02	.6302	.9958	.9991	1.0000	.9993	.9976	.9951	.9922	.9888
.03	.6499	.9917	.9969	.9993	1.0000	.9995	.9981	.9961	.9936
.04	.6678	.9870	.9937	.9976	.9995	1.0000	.9996	.9985	.9968
.05	.6840	.9819	.9901	.9951	.9981	.9996	1.0000	.9997	.9987
.06	.6989	.9766	.9860	.9922	.9961	.9984	.9996	1.0000	.9997
.07	.7126	.9713	.9818	.9889	.9937	.9968	.9987	.9998	1.0000

[2] $\tau = 0$ is Method 2

over the range $0 \leq T \leq .07$, but was relatively more efficient than in 1952. Letting E denote the efficiency of method 1 (means), then, as T rises from zero to .07, in:

1952, E rises from .5836 to .7126,
1953, E rises from .9142 to .9615,
1954, E rises from .9046 to .9587,
1955, E rises from .9370 to .9682, and
1956, E rises from .8058 to .8703.

Table 3 gives a direct comparison of the relative efficiencies of methods 1 and 2 when large values of T are involved, which may, but do not necessarily, arise when maternal effects, non-additive genetic effects, and/or environmental correlations are present. It is interesting to note that the T-value at which the two methods are equally efficient varies considerably due to differences in the distribution of dam family sizes, varying from approximately $T = .09$ in 1953 to $T = .32$ in 1952. The corresponding values of $\psi(T)$, the coefficients of variation of the optimum weights w_{ij}^*, show much more year-to-year stability, however, ranging from a low of .23 in 1953 to a high of .27 in 1952.

Let T_0 represent the value of T for which the two methods are equally efficient. The values $\psi(T_0)$ will not ordinarily be limited to as small a range as observed here (see Table 4). It is quite possible to have much lower values of $C.V.(n)$, which is an upper bound for $\psi(T_0)$. Hence one cannot claim any invariance properties for $\psi(T_0)$. On the

TABLE 3

RELATIVE EFFICIENCIES OF METHODS 1 AND 2 FOR LARGE VALUES OF T.

Year	Method	.10	.20	.30	.40	.50
1952	1(Means)	.748	.825	.870	.900	.920
	2($\tau = 0$)	.956	.912	.880	.856	.838
1953	1(Means)	.970	.984	.990	.993	.995
	2($\tau = 0$)	.963	.932	.912	.898	.889
1954	1(Means)	.968	.984	.990	.993	.995
	2($\tau = 0$)	.971	.947	.932	.921	.914
1955	1(Means)	.974	.985	.990	.993	.995
	2($\tau = 0$)	.974	.952	.937	.926	.918
1956	1(Means)	.887	.924	.945	.958	.966
	2($\tau = 0$)	.975	.945	.920	.901	.885

TABLE 4

ILLUSTRATION OF THE UTILITY OF $\psi(T)$ IN CHOOSING BETWEEN METHODS 1 AND 2.

Year	$\hat{T}$	$\psi(\hat{T})$	$\psi(T_0)$	Estimated Standard Error	
				Method 1	Method 2
1952	.059	.55	.27	.121	.102
1953	.029	.34	.23	.085	.083
1954	.051	.30	.24	.152	.148
1955	.055	.33	.26	.086	.084
1956	.034	.46	.24	.108	.094

basis of information available the recommended procedure for selecting an estimation technique is as follows:

A. From previous experience, or by any other reasoning, assume a value τ for T.

B. If possible, use the Kempthorne-Tandon technique, constructing weights using this assumed value τ.

C. If it is neither possible nor convenient to use method 3, compute $\psi(\tau)$. For large values of $\psi(\tau)$ (say $> .4$) preference is for method

2 whereas for small values of $\psi(\tau)$ (say $< .1$) method 1 is preferred. For intermediate values of $\psi(\tau)$ there should be no substantial differences between methods one and two.

To illustrate the use of this approach, consider Table 4. Here, estimates of T, obtained by Bohren *et al.* [1961], for each of the years 1952–1956, are used to calculate $\psi(\hat{T})$. For comparison, $\psi(T_0)$ is also entered, together with the estimated standard errors of $\hat{\beta}$. The values $\psi(T_0)$ indicate a preference for method 2 in each case, but T_0 is obtained only after tedious calculation. The rule of thumb suggested would lead to strong preference for method 2 in 1952 and 1956 and no preference in the other years.

The results of these investigations indicate that in many circumstances a poor choice of technique can result in serious loss in efficiency in the estimation of β, and thus of heritability in the narrow sense ($h^2 = 2\beta$).

It would seem that, once the expense of experimentation and data collection has been incurred, the investigator is under an obligation to obtain highly efficient estimates. However, in some instances the loss in efficiency is negligible if one of the two standard techniques is used. The use of $\psi(\tau)$ to aid in the choice between the standard methods seems promising.

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SOME HYPOTHESES CONCERNING TWO PHASE REGRESSION LINES

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1. INTRODUCTION

The regression of a growth measurement y on time x can often be reasonably represented by two intersecting straight lines, one being appropriate when x takes values below and the other when x takes values above a certain fixed but often unknown value corresponding to the intersection. Such regressions are here called two-phase regressions, the intersection of the phases being referred to as the *change-over point*, and the value of x at which it occurs being called the *change-over value*.

Situations in which such regressions might occur include the onset of a disease resulting in a reduced growth rate; the application of a treatment having an immediate stimulating or inhibiting effect; the occurrence of an extremely hot or cold day or some other change in external conditions; physical injury of an organism.

In a study of the compatibility of peach scions on plum rootstocks Garner and Hammond [1938] noted that the peach variety Hale's Early developed at constant but different rates on compatible and incompatible rootstock-scion unions up to a certain date. After that date the growth rate in the compatible case continued at a new constant rate, whilst in the incompatible case all growth then ceased.

Thus for a compatible union there was a typical two-phase regression, whilst for the incompatible union a rather special case occurred in which the slope of the second phase was zero. A further example is given in Section 4 in which the date of phase change in relation to time elapsed after application of treatments is of interest.

If x and y are growth measurements on two different parts of the same organism, and Huxley's allometric growth law operates (i.e. there is a linear relation between $\log x$ and $\log y$) it has sometimes been found that sudden changes in slope occur. Reeve and Huxley [1945] have discussed this situation with reference to changes in growth equilibrium in crustacea at sexual maturity. Skellam *et al.* [1959] also

refer to such phase changes in allometric growth, mentioning earlier work of Teissier on this subject.

A biologist will often postulate a two-phase linear regression rather than some alternative such as a parabolic one on largely intuitive grounds, and his decision on this point must be to some extent a matter of experience and common sense, as is generally the case in selecting appropriate hypotheses and models for statistical examination. In many cases a two-phase regression can only be a reasonable approximation, adequate for many purposes, but by no means a complete description of what is taking place.

It is likely that two-phase regressions also arise in economic and in industrial production problems.

2. HYPOTHESES

In the present context questions of the following type are likely to interest the experimenter.

A. Necessity for, and adequacy of, a two-phase fit.

B. Investigation of change-over points and values for individual regressions.

C. Relationships between lines within each phase for several regressions.

D. Relative positions of change-over points for several regressions.

For example, interest may attach to one or more of the following hypotheses.

In relation to *A*:

AI. One phase adequate (i.e. a conventional linear regression suffices),

AII. A two-phase linear regression is adequate;

In relation to *B*:

BI. The observed change-over value is consistent with a specified theoretical value $x = \gamma$;

In relation to *C*:

CI. The lines within a phase are all parallel to one another,

CII. The lines within a phase all coincide;

In relation to *D*:

DI. The change-over points are collinear, all lying on a specified line $y = \alpha + \beta x$, (or $x = \gamma$ if β infinite),

DII. As for *DI* except that α (or γ) not specified,

DIII. The change-over points are collinear on an unspecified line.

In practice, anyone accepting *AI* would proceed no further in this contest. If *AI* were rejected and *AII* accepted, a test of *BI* might be required, and with more than one set of data an experimenter may wish

to proceed to some of the C or D hypotheses. For instance, he might test and accept CI, reject CII as the result of a test (or without test if he considered it incompatible with his data) and then test and accept DII for the case of infinite slope. If x were a time measure, acceptance of DII with β infinite would imply that all phase changes occured at the same time, and is thus likely to be of practical interest. If one wants to know if a phase change can be associated with an event occurring at a particular x value, such as the application of a treatment, or the occurrence of a very hot day, a test of BI is required.

The above hypotheses are by no means exhaustive. Concurrence within a phase, for instance, may be of more interest than parallelism.

In this paper two assumptions that will be made are (i) the classical regression assumption that within each phase the observed y are normally distributed with mean zero and standard deviation σ about the true regression line, and (ii) that it is known between which two observed x the change-over occurs, but not precisely where between these two values it occurs.

This latter assumption calls for some comment. As will be seen, it leads to certain simple tests, and in many practical cases it is not unreasonable. Sometimes observations can only be taken at widely spaced x-values, and it may be clear that the change-over has occurred between two such observations, without a more precise statement being immediately possible.

A difficulty arises if lines are fitted to each phase making the assumption (ii), and the intersection of the fitted lines has an x co-ordinate falling outside the assumed range. The experimenter must then decide whether to attribute this to sampling errors, or an incorrect assumption, and determine the appropriate procedure accordingly. This matter is not pursued further here.

If the second assumption cannot be made because of doubt about the allocation of a small proportion of points near the change-over, the author conjectures that the methods of Quandt [1958] could be used to allocate these doubtful points without seriously upsetting the procedures suggested here. Quandt deals with the allocation problem for a two-regime y-on-x regression where the x occur in a known order with respect to a time measure t, and the phase change occurs when a certain t-value is reached. In the present case $x = t$.

This paper deals mainly with questions classified under B and D, but we first briefly discuss hypotheses involving A and C.

If one has an independent estimate of error variance, the test of AI is simple and standard, being a test for significance of deviations from regression. If deviations from regression provide the only estimate of

error variance and indicate significance of linear regression, some judgement is needed to decide whether a two-phase regression (or any other fit such as a quadratic regression for example) is worth considering. The test of *AII* is likewise essentially a test of the adequacy of two linear regressions, one in each phase.

If *AII* is accepted for more than one set of data and tests for parallelism or coincidence (*CI*, *CII*) are required, these may be performed by standard methods for each phase separately.

We now consider other tests.

3. TESTS

Throughout summations over r run from 1 to 2 (corresponding to the two phases); those involving s run from 1 to n (corresponding to n sets of two-phase regressions); those involving k run from 1 to m_{rs} for the appropriate set and phase, m_{rs} being the number of observations in the rth phase of the sth set. Where it is obvious how many equations (usually 2, n or $2n$) of a given form exist, only typical ones are given.

The first test considered is that of *BI*, that is compatibility with a fixed change-over value, assuming *AII*. The test is based on the comparison of the fit by standard regression techniques of unconstrained lines in each phase, with that obtained if the lines are constrained to intersect at a point whose x co-ordinate γ is given.

Appropriate models for the first and second phases respectively are $E(y) = \alpha_1 + \beta_1 x$ and $E(y) = \alpha_2 + \beta_2 x$, where the constraint to give an intersection at $x = \gamma$ is $\alpha_2 - \alpha_1 + \gamma(\beta_2 - \beta_1) = 0$.

In view of the regression assumptions the method of least squares is appropriate, and a_1 , a_2 , b_1 , b_2 , the estimators of α_1 , α_2 , β_1 , β_2 , are to be determined so as to minimize

$$\sum_r \sum_k (y_{rk} - a_r - b_r x_{rk})^2$$

subject to

$$a_2 - a_1 + \gamma(b_2 - b_1) = 0. \tag{1}$$

Although not essential, introduction of a Lagrange multiplier λ preserves a certain symmetry, and gives rise to many expressions similar to familiar regression results, together with adjustment terms. With such a multiplier the function to be minimized becomes

$$L_1 = \sum_r \sum_k (y_{rk} - a_r - b_r x_{rk})^2 + 2\lambda[a_2 - a_1 + \gamma(b_2 - b_1)],$$

whence, computing the partial derivatives, normal equations are ob-

tained which can easily be reduced to the form

$$\sum_k (y_{rk}x_{rk} - a_r x_{rk} - b_r x_{rk}^2) + (-1)^{r-1}\lambda\gamma = 0, \qquad (2,3)$$

$$a_r = y_{r.} - b_r x_{r.} + (-1)^{r-1}\lambda/m_r , \qquad (4,5)$$

where $y_{r.} = \sum_k y_{rk}/m_r$, etc., m_r being the number of observations in the rth phase. The remaining normal equation is (1). Subtracting (4) from (5) and using (1) gives

$$\lambda = w[d + b_1(x_{1.} - \gamma) - b_2(x_{2.} - \gamma)],$$

where $w = m_1m_2/(m_1 + m_2) = m_1m_2/m$, say, and $d = y_{2.} - y_{1.}$.

Substituting for a_1 , a_2 , λ as given by (4) to (6) in (2) and (3) gives, upon writing Cx_ry_r , Cx_r^2 , etc., for the ordinary corrected sums of products and squares,

$$(e.g.\ Cx_1^2 = \sum_k (x_{1k} - x_{1.})^2, \quad \text{etc.}):$$

$$[Cx_1^2 + w(x_{1.} - \gamma)^2]b_1 - w(x_{1.} - \gamma)(x_{2.} - \gamma)b_2 = Cx_1y_1 - w\,d(x_{1.} - \gamma),$$

$$- w(x_{1.} - \gamma)(x_{2.} - \gamma)b_1 + [Cx_2^2 + w(x_{2.} - \gamma)^2]b_2 = Cx_2y_2 + w\,d(x_{2.} - \gamma).$$

Having solved these equations for b_1 and b_2 it is easy to obtain values for a_1 , a_2 , λ if required from (4), (5) and (6). This constrained fit is then compared with the unconstrained fit for which of course, the slopes b_r' , $(r = 1, 2)$ are given by $b_r' = Cx_ry_r/Cx_r^2$.

If there are $m = m_1 + m_2$ observations, the sum of squares for departures from unconstrained regressions has $m - 4$ degrees of freedom, two regression coefficients and two means having been estimated. For the constrained fit, the corresponding sum of squares has $m - 3$ degrees of freedom since only three independent parameters have been estimated in view of (1). It is easily shown that the difference, with one degrees of freedom, has a sum of squares given by

$$\sum_r (b_r' - b_r)Cx_ry_r + \lambda d. \qquad (7)$$

This sum of squares may also be obtained by subtracting

$$2\sum_r b_rCx_ry_r - \sum_r b_r^2Cx_r^2 - \lambda^2/w$$

from the unconstrained regression sum of squares. It is worth noting that the constrained lines will no longer in general pass through their respective centres of mass.

An F-test of (7) against an appropriate error variance is required. A significant value indicates a worthwhile improvement in fit if the constraint is removed, and in that event *BI* would normally be rejected for the γ under consideration.

The above test may be extended if there are n sets of data, and given change-over values $\gamma_1 , \cdots , \gamma_n$ postulated, each one associated with a given set. The regression coefficients may be estimated separately for each set by the procedure above, using the appropriate constraint each time. If desired, a joint test of the fit compared to unconstrained fits for all sets within each phase may be made. The sum of squares (7) is computed for each set, and these are added together to give a sum of squares with n degrees of freedom which can be tested against an appropriate error variance. If $\gamma_1 = \cdots = \gamma_n$ it will be noted that this test is essentially a test of *DI* with β infinite.

Turning now to *DII* there is little difficulty in developing a test if the change-overs are assumed to lie on a line of infinite slope (i.e. to occur at the same unknown x-value) providing *AII* and *CI* are accepted (i.e. all lines within each phase are parallel to one another). It will be assumed that all lines in the first phase have the same slope b_1 , and all lines in the second phase have the same slope b_2 , $(b_1 \neq b_2)$. A comparison has to be made between a fit constrained so that all change-over points lie on a line $x = \gamma'$, and a fit not so constrained. (Note γ' is not specified, and must be estimated.)

The model now is

$$E(y) = \alpha_{1s} + \beta_1 x \quad \text{and} \quad E(y) = \alpha_{2s} + \beta_2 x$$

for the respective phases, where $s = 1, \cdots , n$, and there are n constraints which may be written

$$\alpha_{2s} - \alpha_{1s} + \gamma'(\beta_2 - \beta_1) = 0. \tag{8}$$

As β_1 , β_2 and γ' are independent of s, it is convenient to replace (8) by the n constraints

$$\alpha_{2s} - \alpha_{1s} = \gamma,$$

the geometrical significance of which, in relation to intercepts, is obvious. The function to be minimized in order to estimate these parameters (including γ in this case) is

$$L_2 = \sum_r \sum_s \sum_k (y_{rsk} - a_{rs} - b_r x_{rsk})^2 + 2 \sum_s \lambda_s (a_{2s} - a_{1s} - c),$$

the λ_s being Lagrange multipliers. Differentiation gives rise to a set of normal equations, e.g.

$$\sum_s \sum_k (y_{rsk}x_{rsk} - a_{rs}x_{rsk} - b_r x_{rsk}^2) = 0,$$

$$a_{rs} = y_{rs.} - b_r x_{rs.} + (-1)^{r-1}\lambda_s/m_{rs},$$

$$\sum_s \lambda_s = 0,$$

$$a_{2s} - a_{1s} - c = 0. \tag{9}$$

These lead, after some straight-forward but tedious algebra to the equations

$$c = {}_w y_{2..} - b_{2w}x_{2..} - ({}_w y_{1..} - b_{1w}x_{1..}), \tag{10}$$

$$[\sum Cx_{1s}^2 + C_w x_{1.}^2]b_1 - C_w x_{1.}x_{2.}b_2 = \sum Cx_{1s}y_{1s} - C_w x_{1.}\, d, \tag{11}$$

$$-C_w x_{1.}x_{2.}b_1 + [\sum Cx_{2s}^2 + C_w x_{2.}^2]b_2 = \sum Cx_{2s}y_{2s} + C_w x_{2.}\, d, \tag{12}$$

where Cx_{rs}^2, $Cx_{rs}y_{rs}$ are the usual corrected sums of squares and products for the sth line of the rth phase, and

$$\begin{aligned}
{}_w y_{r..} &= \sum w_s y_{rs.} / \sum w_s, \\
{}_w x_{r..} &= \sum w_s x_{rs.} / \sum w_s, \\
w_s &= m_{1s}m_{2s}/(m_{1s} + m_{2s}), \\
C_w x_{r.}^2 &= \sum w_s x_{rs.}^2 - {}_w x_{r..}(\sum w_s x_{rs.}), \\
C_w x_1 . x_2 . &= \sum w_s x_{1s.}x_{2s.} - {}_w x_{1..}(\sum w_s x_{2s.}), \\
C_w x_1 .\, d &= \sum w_s x_{1s.}\, d_s - {}_w x_{1..}(\sum w_s\, d_s), \\
d_s &= y_{2s.} - y_{1s.}, \quad \text{etc.}
\end{aligned}$$

In the above all summations are over s.

It is easiest to solve (11) and (12) for b_1 and b_2, then obtain c from (10). For testing purposes it is convenient to know the λ_s, which can be obtained from the easily deducible relations

$$\lambda_s = w_s(d_s - b_2 x_{2s.} + b_1 x_{1s.} - c). \tag{13}$$

Putting $m = \sum_r \sum_s m_{rs}$, the total number of observations, then for unconstrained parallel lines the sum of squares for deviations from regression has $m - 2n - 2$ degrees of freedom. When the constraints (8) apply we fit only $n + 3$ independent parameters and thus have $m - n - 3$ degrees of freedom for deviations from regression. The difference between these two deviation sums of squares has $n - 1$ degrees of freedom, and is obtained as

$$\sum_r \sum_s (b_r' - b_r)Cx_{rs}y_{rs} + \sum_s \lambda_s\, d_s, \tag{14}$$

where b_1' , b_2' are the regression coefficients for unconstrained parallel lines.

Equations (11) and (12) simplify somewhat if the x's are the same for all sets of data.

4. EXAMPLE

R. M. Fulford (personal communication) has made counts of the number of nodes in terminal buds of spurs of the apple variety Miller's seedling from the first or outermost budscale to the youngest primordium at intervals after the application of three defoliation treatments. The treatments were applied on different dates, and the counts were made at intervals of seven or more days throughout the 1957 growing season. On each counting date at least six buds from trees that had received a given treatment were examined. The counting dates were not always the same for all treatments, but were generally close together and covered a comparable time span.

The regression of y, the number of nodes, upon x, the number of days after May 24th, was found to be consistent with the hypothesis of three sets of two-phase parallel regressions (i.e. *AII* and *CI* were satisfied). This was tested by standard methods which are not reproduced here. It appeared from the data that the change-overs might well have occurred on the same calendar date, rather than at, say, the same fixed number of days after the application of each treatment. In each phase of each regression there were observations for between six and eleven distinct counting dates x.

The raw data are not reproduced here; but relevant means, sums of squares and products, weights, etc., are given.

The content of Table 1 was computed directly from the data, and that of Table 2 from that of Table 1.

The coefficients in equations (10) to (12) are easily got from these tables, and give

$$c = 8{\cdot}260 - 97{\cdot}856b_2 + 39{\cdot}578b_1 ,$$

$$56926{\cdot}21b_1 - 777{\cdot}54b_2 = 11388{\cdot}08,$$

$$-777{\cdot}54b_1 + 19057{\cdot}96b_2 = 954{\cdot}93,$$

whence $b_1 = 0.2008$, $b_2 = 0.0583$, $c = 10.502$. From (13) we then get

$$\lambda_1 = -4{\cdot}404, \qquad \lambda_2 = -5{\cdot}611, \qquad \lambda_3 = 10{\cdot}017.$$

The λ_s , apart from rounding errors, sum to zero, providing a useful check. Computing (14) we find it comes to 7.32. This sum of squares has 2 degrees of freedom. An appropriate error mean square is provided

TABLE 1.

MEANS, SQUARES, PRODUCTS, WEIGHTS

s	$x_{1s.}$	$x_{2s.}$	$y_{1s.}$	$y_{2s.}$	d_s	Cx_{1s}^2	Cx_{2s}^2	$Cx_{1s}y_{1s}$	$Cx_{2s}y_{2s}$	w_s
1	35.27	94.50	16.62	25.36	8.74	31345.09	5145.00	6335.82	360.50	23.29
2	38.62	98.00	16.48	24.69	8.21	12059.25	8232.00	2488.62	455.00	22.40
3	45.50	101.50	17.04	24.81	7.77	12348.00	5145.00	2457.00	213.50	20.57
					Sums	55752.34	18522.00	11281.44	1029.00	66.26

TABLE 2.

COMPUTATIONS REQUIRED FOR COEFFICIENTS IN NORMAL EQUATIONS

s	$w_s x_{1s.}$	$w_s x_{2s.}$	$w_s d_s$	$w_s x_{1s.}^2$	$w_s x_{2s.}^2$	$w_s x_{1s.} x_{2s.}$	$w_s x_{1s.} d_s$	$w_s x_{2s.} d_s$
1	821.44	2200.90	203.55	28972.19	207985.05	77626.08	7179.21	19235.87
2	865.09	2195.20	183.90	33409.78	215129.60	84778.82	7102.39	18022.20
3	935.94	2087.86	159.83	42585.27	211917.79	94997.91	7272.27	16222.67
sums	2622.47	6483.96	547.28	104967.24	635032.44	257402.81	21553.87	53480.74
wt. mean	39.578	97.856	8.260					
Weighted correction				103793.37	634496.48	256625.27	21660.51	53554.81
Weighted corrected SS or SP				1173.87	535.96	777.54	−106.64	−74.07

by that between counts on the same date within treatments and has the value 1.08 with 230 degrees of freedom. This routine computation is not shown. The appropriate F is thus $3.66/1.08 = 3.39$, and this is significant at the 0.05 probability level. Thus there is evidence for rejecting the hypothesis of a common change-over date, although it was clear from the data that the change-overs occurred nearer to a common calendar date than they did to a constant time lapse after application of each treatment. In the computations, particularly in calculating (14), care is needed to avoid excessive rounding errors.

5. RELATION TO FIELLER'S THEOREM

It is evident that a test of consistency of the observed change-over value with a specified $x = \gamma$, (hypothesis BI) is equivalent to a test about the intersection of two regression lines, and the test developed in Section 3 might be expected to be related to Fieller's [1940, 1944] theorem on fiducial limits of a ratio. Fieller has shown that the fiducial limits for $\theta = y/x$, where the errors in y and x are normally distributed with zero mean, are given by the roots of the quadratic in θ

$$(y^2 - t^2 v_{yy}) - 2\theta(xy - t^2 v_{xy}) + \theta^2(x^2 - t^2 v_{xx}) = 0,$$

where v_{yy} , v_{xx} , v_{xy} are estimates of the variances and covariance of y and x, each based on n degrees of freedom, and t is the appropriate value of Student's t for the required fiducial probability with n degrees of freedom.

Applying the theorem in the situation envisaged in BI, Fieller's $y = a_2' - a_1'$, and his $x = b_1' - b_2'$, in terms of the parameters of unconstrained regression lines. The estimated variances and covariances of these, using an appropriate error mean square s^2 say, are easily obtained. On the criterion of Section 3 for testing BI, a chosen γ will just be significant if

$$\sum_r (b_r' - b_r)Cx_r y_r + \lambda d - t^2 s^2 = 0. \qquad (15)$$

From Fieller's theorem it follows that such a γ is given as a root of the quadratic in γ,

$$[\gamma(b_1' - b_2') - (a_2' - a_1')]^2 - t^2 s^2 \cdot \left[\frac{1}{w} + \frac{(x_{1\cdot} - \gamma)^2}{Cx_1^2} + \frac{(x_{2\cdot} - \gamma)^2}{Cx_2^2}\right] = 0. \qquad (16)$$

The left-hand side of (15) can be shown to be a quadratic in γ, and thus (15) and (16) will be equivalent if it can be shown that their left-hand sides are identical for three distinct values of γ. This is easily done when $\gamma = x_{1\cdot}$ or $x_{2\cdot}$ or $(a_2' - a_1')/(b_1' - b_2')$.

Thus using Fieller's theorem to establish fiducial limits for γ provides a set of γ's (i.e. those between the limits) which would be acceptable under the hypothesis test put forward here.

With either Fieller's theorem, or the approach used here, difficulties arise if γ is infinite, but in practice this causes no trouble in the present context as an infinite γ would imply the identity of the two phases, i.e. acceptance of *AI*, or alternatively a pair of parallel regressions, rather than the abrupt change of slope implied by γ finite.

Whilst Fieller's theorem does not link directly with the test already considered for a common unspecified change-over date for all of n sets of data, it does provide a solution to a closely related problem, namely:

Assuming there is a common-change over date, what are the p percent fiducial limits for this? Equations (10) to (12) provide estimates c, b_1 , b_2 , of γ, β_1 , β_2 respectively. The γ' of (8) is related to γ by the expression

$$\gamma = (\beta_1 - \beta_2)\gamma',$$

thus γ' may be estimated as

$$c' = c/(b_1 - b_2). \tag{17}$$

If the value of c given by equation (10) is put in (17) and the variances and covariance of numerator and denominator obtained in the usual way, Fieller's theorem may be applied.

6. DISCUSSION

An important characteristic of the tests derived in Section 3 is that they involve linear constraints upon the parameters. This would not be the case for instance if one wished to test *DII* with β infinite but without the restriction to parallelism introduced in Section 3. Then the n constraints would become

$$a_{2s} - a_{1s} = c(b_{1s} - b_{2s}),$$

all terms being unknown. Further, if one wished to test *DII* with β finite, and no restriction to parallelism, the constraints would take the form

$$b_{1s}a_{2s} - b_{2s}a_{1s} = \alpha(b_{1s} - b_{2s}) + \beta(a_{2s} - a_{1s}).$$

These do not easily reduce to a workable system of linear constraints and we are consequently led to non-linear normal equations. It is seldom that such equations can be easily reduced to a linear set, and iterative solutions or other special methods are required. Similar difficulties arise with many hypotheses associated with problems of type *D*.

An alternative approach to questions of linearity of the change-over points might be via the fitting of lines to the observed unconstrained change-over points. As these will almost certainly be determined with different accuracies for different sets of data depending upon the numbers of points, and their positionings, in each phase, some weighting process is indicated, and the approach is entirely different from that adopted here.

Finally, from the biological viewpoint it must be emphasised that the ability to use techniques of the type suggested here in no way reduces the need for the experimenter to consider the biological reasonableness of the model he uses, and whether it is more than a convenient approximation.

7. ACKNOWLEDGEMENTS

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QUERIES AND NOTES

D. J. FINNEY, *Editor*

165 NOTE: A Practical Application of a Theoretically Inefficient Design[1]

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1. INTRODUCTION

In experiments on milking machine techniques for reducing the time taken to milk each cow, it was desired to compare milking times given by combinations of two pulsation ratios, P_1 and P_2 with two levels, V_1 and V_2, of vacuum in the machine line. It was expected (see Section 3) that the animal to animal variability would differ substantially for the different treatments, in view of which, and the short time available for the experiment, it was decided to limit the experiment by having only two treatments per animal. The main restriction determining the design arose because the treatment combination P_1V_1 was of such special interest that it was desired to obtain an estimate of the corresponding milking time from all the available animals. The simple solution used nicely illustrates the dual features of estimation and discrimination which often interplay in biological operational research.

2. DESIGN PRINCIPLES

Each animal formed an incomplete block receiving two of the four possible treatment combinations with four successive observations on each. The special feature is that, to provide the estimate required, all animals received the combination P_1V_1 and practical considerations made it necessary for this to be the treatment for each animal in the first period. In theory therefore, the treatment differences would be confounded with any period differences but, in this case, previous experience had shown that these could safely be discounted in such a

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short experiment. It was logical therefore to allot the three remaining treatment combinations equally, and randomly, to the animals in the second period. Thus, if P_1V_1 is regarded simply as a control, the design itself is that properly deprecated by Yates [1936] for cases when treatment differences only are required, because of its inefficiency relative to the arrangement using all the six possible pairs. This latter design was inadmissible here because of the primary estimation requirement and it will appear that, because every observed difference contributes to each, the main effects of treatments and the interaction are estimated with sufficient accuracy to give discrimination at a useful practical level.

3. ANALYSIS

Let d_{ij} be the difference between the two period means for the jth animal on the treatment arrangement distinguished by the suffix i, as follows:

period	1	2
$i = 1$	P_1V_1	$-P_2V_1$
$i = 2$	P_1V_1	$-P_1V_2$
$i = 3$	P_1V_1	$-P_2V_2$

and $j = 1, \cdots, n$ for each i.

Let $d_{i.}$ be the mean of d_{ij} over the n animals receiving the ith arrangement. Then the treatment comparisons are estimated as:

	$d_{1.}/2$	$d_{2.}/2$	$d_{3.}/2$
main effect of $P = \frac{1}{2}(P_2 - P_1)(V_1 + V_2)$	-1	1	-1
main effect of $V = \frac{1}{2}(P_1 + P_2)(V_2 - V_1)$	1	-1	-1
interaction $PV = \frac{1}{2}(P_2 - P_1)(V_2 - V_1)$	1	1	-1

Hence, if σ_i^2 is the variance of an individual d_{ij}, each effect and the interaction is estimated with variance $(\sigma_1^2 + \sigma_2^2 + \sigma_3^2)/4n$.

With n animals in each of the three i-groups separate analyses of the d_{ij} are obtained for each group according to the simple partition:

treatment difference	1
between animals	$(n - 1)$

to which a within animals term may be added if required.

In the example, the mean differences $d_{i.}$ together with the between-animal mean squares with $n = 8$ were:

treatment difference	$d_{i.}$	mean square (7 d.f.)
$P_1V_1 - P_2V_1$	−0.244	0.1467
$P_1V_1 - P_1V_2$	−0.638	1.5225
$P_1V_1 - P_2V_2$	−1.631	1.9339

We thus obtain the main effects and interaction, in minutes, as

$$P = \tfrac{1}{2}(0.244 - 0.638 + 1.631) = 0.619,$$

and similarly,

$$V = 1.012, \qquad PV = 0.375.$$

The appreciable differences between the above three mean squares are noteworthy and were expected because milking times are functions both of the machine variables and their interactions with highly individual characteristics such as the amounts of milk secreted, neurohormonal responses and anatomical details of teats and udders.

The variance of each main effect and of interaction PV is calculated as

$$(0.1467 + 1.5225 + 1.9339)/32$$

giving a standard error of 0.336 minutes.

Since each mean square has the same number of degrees of freedom, the ordinary t-value for seven d.f. can be used for an approximate test of significance (after Cochran and Cox, [1957]) showing here that only the V-effect is significant at the five percent level.

4. DISCRIMINATION VERSUS ESTIMATION

It has been pointed out that the estimation requirement is fulfilled at the expense of the accuracy achieved for the treatment comparisons. Had a design employing all pairs of treatment combinations been applicable there would have been three more treatment groups,

$$i = 4 \quad P_2V_1 - P_1V_2 ,$$

$$i = 5 \quad P_2V_1 - P_2V_2 ,$$

$$i = 6 \quad P_1V_2 - P_2V .$$

The main effect of P, for example, calculated without recovery of inter-animal information, is then,

$$P = -\frac{1}{4}(d_{1.} + d_{3.} - d_{4.} + d_{6.}),$$

and, instead of n, there will now be $n/2$ animals in each group.

The variance heterogeneity in the particular example complicates the direct comparison but, if in a general case, transforming if necessary, we assume that each d_{ij} has variance σ^2, the variance of a treatment comparison is now

$$\frac{4}{16} \cdot \frac{2\sigma^2}{n} = \sigma^2/2n,$$

which compares with $3\sigma^2/4n$ obtained when only three differences are directly investigated.

Both designs provide unbiassed estimates of the milking time on P_1V_1 and the above loss of discrimination is compensated by the fact that this mean milking time is estimated with only half the variance which would have obtained if all the paired differences had been used.

Finally, with reference to the particular example, when not only the mean but the distribution of milking times on the P_1V_1 combination is of interest, the larger numbers of observations obtained with the design used will be additionally advantageous.

5. ACKNOWLEDGEMENTS

I am grateful to F. H. Dodd and M. C. Cowhig for providing the data of this example.

6. REFERENCES

Cochran, W. G. and Cox, G. M. [1957]. *Experimental Designs*. John Wiley & Sons, New York.

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166 QUERY: On a Graphical Sequential Test

Bross [1952] describes a graphical sequential test, and among the plotting rules is the instruction that "if new and old treatments lead to the same outcome then no information about superiority is obtained and nothing is plotted on the chart". From his chart therefore distinguishable results are considered significant whether they are 6 out of 6, or 6 out of 100 in the other 94 of which both treatments gave the same result. If one treatment kills 100 patients, and the other kills

94 and cures 6, normal probability ideas seem to suggest that there is only a 6 percent chance that there is some difference between the treatments, and not that it is less than 5 percent that there is no difference. Is it wise to ignore some of the experimental results? Should the instruction be reworded "if the fact that the outcome of the new and old treatments is the same provides no information towards the particular problem being investigated, nothing is plotted on the chart: if it supports a hypothesis that the treatments are not different, then the experiment is plotted in the square adjoining the last plot diagonally away from the origin"?

REFERENCE

Bross, I. D. J., [1952]. Sequential medical plans, *Biometrics 8*, 188.

ANSWER:

Although the query concerns a sequential procedure it applies equally well to the fixed sample procedure—the Sign Test—which is the parent of this sequential procedure so let us look at the simpler example. Both the Sign Test and its sequential analogue would be based on a study plan where one member of each patient *pair* is randomly allocated to treatment A or B (the second member receiving the remaining treatment). When both patients in the pair have the same response (both live, both die), the "tie" is ignored insofar as the significance test is concerned. Thus in the example of the query the test would be based on the six pairs where the patient on treatment A survived and the patient on B dies (and the zero cases with the opposite results). The Mosteller-Corrected Sign Test would be $(6-1)^2/6=4.17$. This exceeds 3.84 so the results would be significant at the 5 percent level.

Is it wise to ignore some of the experimental results (eg. the "ties")? Let me make it clear that the "ties" would *not* be ignored in other phases of the analysis which deal with the *clinical importance* of the difference between treatments. The question, then, is whether "ties" should be ignored in dealing with the specific point: Is there *any* difference in the responses to the two treatments? There are two technical approaches which will provide an answer to the question. First we might ask: Does ignoring the ties impair the efficiency of the procedure? The technical answer is that the loss of efficiency is negligible. Second we might ask: If significance tests are set up which involve the tied

observations, will they be better than the Sign Test? The technical answer is that there is no advantage to the alternative procedures and sometimes they result in a loss of power. While both technical approaches lead to the answer "ties can be ignored" they may not satisfy an investigator who would like a simple rationale rather than a formal proof.

Therefore I will indicate a rationale for the clinical situation. The purpose of therapeutic intervention is to *change* the natural clinical course of a disease in a favorable direction. Let us suppose treatment B fails to change the natural course (i.e. to death) while treatment A occasionally can change this course. Then the *number of changes* achieved on treatment A constitute the evidence of a difference between the two treatments. If there are 6 changes, we have the same amount of evidence of a difference whether it comes from 6 pairs or 600 pairs. If there were some spontaneous remissions (eg. not due to treatment), then we would have to compare the number of changes in the two series but *this* information' would constitute the available evidence of a difference between the two treatments (irrespective of the number of pairs). When our interest lies in change of status then the "ties" are irrelevant.

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167 NOTE: A Simple Method of Fitting the Regression Curve $y = \alpha + \delta x + \beta\rho^x$

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Patterson [1956] described a simple method for fitting an asymptotic curve

$$y = \alpha + \beta\rho^x, \qquad x = 0, 1, \cdots, n-1, \tag{1}$$

for $n = 4, 5, 6$ and 7 equally spaced ordinates. In this method ρ is estimated by r, the ratio of two linear functions of y's and α and β can be obtained by the linear regression of y on r^x.

This method can be extended to the problem of fitting the curve

$$y = \alpha + \delta x + \beta\rho^x \tag{2}$$

for equally spaced ordinates. Here also the estimate of r is a ratio of two linear contrasts of the y's and the estimates α, δ and β are calculated from a multiple linear regression of y on x and r^x.

As four parameters are to be estimated, the above method gives an exact fit for $n = 4$ using the formula

$$r = \frac{y_3 - 2y_2 + y_1}{y_2 - 2y_1 + y_0}. \tag{3}$$

The following formulae are suggested for $n = 5, 6, 7$ and 8:

$$r = \frac{5y_4 - 4y_3 - 7y_2 + 6y_1}{5y_3 - 4y_2 - 7y_1 + 6y_0}, \quad \text{for} \quad n = 5, \tag{4}$$

$$r = \frac{10y_5 - y_4 - 13y_3 - 11y_2 + 15y_1}{10y_4 - y_3 - 13y_2 - 11y_1 + 15y_0}, \quad \text{for} \quad n = 6, \tag{5}$$

$$r = \frac{10y_6 + y_5 - 6y_4 - 14y_3 - 8y_2 + 17y_1}{10y_5 + y_4 - 6y_3 - 14y_2 - 8y_1 + 17y_0}, \quad \text{for} \quad n = 7, \tag{6}$$

and

$$r = \frac{10y_7 + 5y_6 - 5y_5 - 12y_4 - 11y_3 - 7y_2 + 20y_1}{10y_6 + 5y_5 - 5y_4 - 12y_3 - 11y_2 - 7y_1 + 20y_0}, \quad \text{for } n = 8. \tag{7}$$

Then four formulae are chosen to give a reasonably high efficiency for independent y's with equal variances. The percentage efficiencies for $n = 5, 6, 7$ and 8, calculated from large sample formula for the variances of r and the efficient estimate (Shah and Patel, [1960]), are:

ρ	$n = 5$	$n = 6$	$n = 7$	$n = 8$
0.0	95.2	91.3	88.4	86.4
0.1	98.4	97.3	96.0	94.4
0.2	99.7	99.7	99.0	97.8
0.3	99.9	99.7	98.4	96.9
0.4	99.6	98.4	95.5	93.0
0.5	99.0	96.1	91.4	87.5
0.6	98.1	93.7	87.1	82.6
0.7	97.3	91.4	83.0	76.1
0.8	96.3	89.4	79.1	71.8
0.9	95.4	86.7	75.9	68.2

Thus the efficiencies of the proposed estimates are of about the same order as the efficiencies of Pattersons estimates of ρ for equation (1).

REFERENCES

Patterson, H. D. [1956]. A simple method for fitting an asymptotic regression curve. *Biometrics 12*. 323–29.

Shan, B. K. and Patel, I. R. [1960]. The least square estimates of the constants for the Makeham second modification of Gomperts's Law. *Jour. Maharaja Sayojirao University of Baroda 1*, Vol. IX. No. 2. 1–10.

168 QUERY: On a Follow-up Study of the Growth of Children

In conducting a long term follow-up study of the growth and development of a sample of children, the question arises as to whether losses between birth and 4 years were such as to bias the remaining sample. Two specific questions may be asked:

(a) Are losses independent of social class, age of parent etc? Leavers and stayers were compared, on several variables, using the Brandt-Snedecor method for a $2 \times k$ table.

Example

Mother's age at child's birth	Initial Sample	Leavers	Stayers (X)	Proportion remaining (p)	pX
up to 24	49	18	31	.6327	19.6137
25–32	117	25	92	.7863	72.3396
33+	55	6	49	.8909	43.6541
Totals	221	49	172	$\bar{p} = .7783$	$\sum pX = 135.6074$
					$\bar{p} \sum X = 133.8676$
					diff. = 1.7398

$$\chi^2 = (\sum pX - \bar{p} \sum X)/\bar{p}\bar{q} = 1.7398/.1725$$
$$= 10.09 \qquad (.01 > P > .001).$$

With several parental and social variables, χ^2 indicated significant differences between leavers and stayers.

(b) What is the probability that the remaining sample (stayers) could arise by random sampling from the original sample?

This would involve not a test of independence between staying and mothers' age, but a test of the difference between observed frequencies

among stayers, and expected frequencies based on the proportions in the original sample.

Can χ^2 be used to answer this question? It would seem illegitimate, in so far as expected values would themselves be derived from sample values, and not from population values.

Douglas and Blomfield (1) employed a χ^2-test in this way, but in their case the initial sample consisted of all children born in a particular week in the majority of local authority areas of England and Wales. They derived expected frequencies in social class categories from the proportions in this sample, and applied them to the stayers. Is this legitimate, in so far as their expected frequencies might be said to be derived from population values?

If the χ^2-technique is inapplicable in my case, is there any other way of assessing how unrepresentative the remaining sample has become?

REFERENCE

Douglas, J. W. B. and Blomfield, J. M. [1956]. The reliability of longitudinal surveys. *Milbank Mem. Fund Quart. 34*, 227–252.

ANSWER:

Since the original sample was random, the two questions, "Are the proportions of 'leavers' and 'stayers' effectively the same in the different rows?", and "Can the sample of stayers be regarded as a random sample of the original population?" are equivalent. The χ^2-test answers the question "Could the samples in all rows (or all columns) of the table have arisen by random sampling from a single population?", which is a slightly more specific version of the first question above. Since for your data χ^2 is significant, we are led to conclude that there is a genuine difference in the proportions of mothers of different ages in the sub-populations of 'all stayers' and 'all leavers' (i.e. of all mothers in the population who would have been classified under these headings had they been included in the sample): since the original sample was random, the sample of stayers must be regarded as having been drawn at random from the sub-population of all stayers, and so cannot be regarded as randomly drawn from the whole population. No independent test of this is necessary, or indeed possible: since the two questions are logically equivalent, the same test must be used to answer both. Admittedly it appears at first sight that a different test could be derived by com-

paring the observed numbers of stayers with their expectations, using the statistic

$$\chi^2 = \sum \frac{[X_i - E(X_i)]^2}{\text{Var}\,(X_i)}, \tag{1}$$

where X_i is the number of stayers in the ith class, and the expectation and variance of X_i are calculated on an appropriate null hypothesis. This statistic does not appear to depend on the numbers of leavers: however, since the true population proportions are here unknown, this test can only be based on the null hypothesis that the X_i have arisen by independent random binomial sampling from the small numbers n_i of the original sample, with a common probability estimated by $\bar{p}$. Hence Var (X_i) must be estimated by $n_i\bar{p}\bar{q}$, so that formula (1) yields

$$\chi^2 = \sum \frac{[X_i - n_i\bar{p}]^2}{n_i\bar{p}\bar{q}},$$

which, after a little manipulation, reduces to precisely the form that you have already used to calculate χ^2. Only if all the values of p are very small, so that $\bar{q}$ can be taken as effectively equal to 1, can formula (1) be approximated by the expression

$$\chi^2 = \sum \frac{[X_i - E(X_i)]^2}{E(X_i)}. \tag{2}$$

For your data $\bar{q} = 0.2217$, so that the use of formula (2) would be illegitimate, as you conjecture, and would give a χ^2 less than one-quarter the size of the correctly calculated value. As far as I am able to judge from the information given in their paper, the test used by Douglas and Blomfield is in fact invalid for this reason.

Having once decided that leavers and stayers do differ we *may* ask, quite legitimately, the further question, "Is the non-randomness of the stayers, regarded as a sample of the original population, sufficiently serious to produce large biases in the estimates to be calculated from the sample?" If the overall proportion of leavers were small, the disturbances introduced by any variation in rate of loss might well be negligible in comparison with the original sampling variation, so that the sample of stayers could be treated as though it were a random sample from the population: the resultant estimates would be biased, but the bias would be unimportant. If the true proportions in the various classes in the population are known, χ^2 may be calculated from formula (2): it must not be regarded as a test statistic, since the appropriate null hypothesis has already been rejected, but its size may be used as a criterion of the degree of non-randomness of the sample of stayers.

If the population proportions are unknown, as in your example, some indication of the seriousness of the risks involved in treating the sample of stayers as random may be obtained by considering the changes produced by leaving in the proportions of the sample falling in the various groups. For example, in the results quoted by Douglas and Blomfield the largest change in any employment group was in that of 'manual workers', which comprised 0.691 of the original sample, and 0.696 of the sample of stayers. Clearly, even though the authors were in error in maintaining that the sample of stayers could be regarded strictly as a random sample from the population, the degree of bias introduced by so regarding it was trivial. In your data, on the other hand, the proportion of mothers under 25 has fallen from 0.222 in the original sample to 0.180 in the sample of stayers, a much more serious change.

Biases resulting merely from the changes in proportions can be largely avoided, in theory, by calculating separate estimates for the different groups, and combining them according to the proportions of the original sample. However, a breakdown of the sample taking into account all criteria that show significant changes in proportions may well leave you with groups too small for satisfactory estimation, and this method cannot allow for the further danger that the leavers will almost certainly be non-typical of the population even within groups, so that a considerable bias may remain even though the effects of disproportionality are successfully removed.

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BOOK REVIEWS

J. G. SKELLAM, *Editor*

Members are Invited to Suggest Books for Listing or Review to the Editor

16 DE JONGE, H. (editor). **Quantitative Methods in Pharmacology.** Amsterdam: North-Holland Publishing Company, 1961. Pp. xx + 391. £4.4s.

D. J. FINNEY, *University of Aberdeen, Scotland.*

In May 1960, the Netherlands Region of the Biometric Society organized a Symposium for the Society. This volume contains the texts of the 26 papers presented, together with summaries of discussions and of remarks by chairmen. The papers differ greatly in interest and importance, and any selection for comment here may reflect the taste of the reviewer as much as the quality and balance of the Symposium.

The first section of the book contains papers on sequential trials of drugs. HAJNAL presents an excellent account of sequential tests of four analgesics against a control, where assessment is in terms of a continuous variate and estimates of effects are wanted. JOHNSON introduces an important subject in a short paper on how to choose a sequential procedure that will meet practical requirements. RÜMKE suggests uses of sequential techniques for estimating doses to be used in a definitive experiment; his idea is incompletely worked out, and questions of efficiency are not discussed, but it may give rise to improvements in the strategy of using pilot experiments.

The second section, on drug standardization, includes a theoretical paper by CLARINGBOLD and EMMENS, consisting of a formal account of computational procedures appropriate to multivariate quantal responses under a general transformation, of which the normal equivalent deviate is a familiar example. Numerical illustration might have been helpful. Additional evidence is given that many types of data are insensitive to the choice of transformation, and the angle transform is therefore commended for general use. VAN STRIK's suggestion of using rank as a metameter for semi-quantitative responses may sometimes be helpful, but the method fails completely in two special cases and one may suspect that other rank orders close to these extremes will give trouble.

Evidently the most controversial session of the Symposium was that on non-parametric methods. HEMELRIJK and VAN DER VAART contribute papers on the efficiency and robustness of Wilcoxon's test; both are of considerable theoretical interest, though neither recognizes that the interpretation of numerical observations can seldom be completed solely by appeal to tests of significance. VAN EEDEN's ingenious but misleadingly titled paper illustrates this well; her method of estimating some points of the distribution function for a tolerance distribution, without assumption of any specified functional form, can evidently be extended to provide a method of estimating relative potency from two series of records which will work for some data, though for others it may be ambiguous. At best, it must be indeterminate to the extent of unit interval on the dose scale, and the author's hopes of finding a method of assigning a measure of precision to such an estimate seems at present to lack foundation. JUVANCZ's entertainingly vigorous attack on

non-parametric methods perhaps relies too much on what users of statistics have done rather than on what they ought to do, but comes closer to the needs of scientific research. In "A Visual Approach to Bio-Assay," GOLDBERG presents an ingenious system of graphs and scales that enable a close approximation to the maximum likelihood estimation of parameters for a quantal response regression to be achieved by a series of additions. The account of this, even for the single parameter exponential model, is so complicated as to make this reviewer prefer the simplicity and speed of standard maximum likelihood calculations.

The sections on drug screening and on mixtures of drugs are of consistently high standard. DUNNETT and SCHNEIDERMAN each discuss problems of evaluating alternative screening rules with emphasis on economic aspects. Dunnett considers carefully the components of cost and loss that must enter into the specification of an optimal screening programme for a large number of drugs by appropriate decision rules; Schneiderman concerns himself more with the operating characteristics of his sequential procedures for screening anticancer drugs, and includes interesting comments on the use of a well-instructed computer. BROCK and SCHNEI DER seek to rehabilitate the therapeutic index by more careful definition than is customary; consideration of optimal experimental planning for the estimation of their index might throw more light on the seriousness of the loss in precision inherent in working at 5% and 95% response rates. Alternative, but not necessarily conflicting, views on quantal responses to mixtures of drugs are discussed by ARIËNS and SIMONIS and by HEWLETT and PLACKETT. The comprehensive mathematical models of the second will have the greater appeal for the statistician; for the pharmacologist, this summary of metrical aspects of Ariën's receptor theory should prove valuable, and perhaps the conjunction of the two will stimulate an effective synthesis. DIKSTEIN's short account of a hypothesis relating chain length of primary and monoquaternary amines to excitation of guinea-pig muscle must surely be the forerunner of much work on the relation of physicochemical properties and pharmacological action. DE JONGH gives a useful and simple summary of the isobole method of representing different types of action of drugs in mixture.

Inevitably a symposium of this kind includes a group of papers that defy any classification other than "miscellaneous", but those in the present volume are not the less interesting for that. GURLAND's suggestions on bioassays for estimation of minute insecticidal residues include useful practical ideas for taking account of the masking of potency by inactive materials present in plant extracts and for the "fortification" of test extracts of very low potency so as to permit adequate assays when available quantities are severely limited. Finally, a contribution from BILLEWICZ describes a statistical study of a technique of measurement (the falling drop technique for estimating the concentration of deuterium oxide): although in itself purely physical, this is a good example of the manner in which a statistician can help to improve the accuracy of a laboratory technique.

17 LE ROY, H. L. **Statistische Methoden der Populationsgenetik.** Stuttgart: Birkhauser Verlag, 1960, pp. 397, 67.5 Swiss Francs.

C. HARTE, *Universität zu Köln, Germany.*

This book contains an extensive description of statistical methods used in modern population genetics. The reader is assumed to have some knowledge of

genetics and general biometrical methods, especially correlation methods and the analysis of variance. The first chapter deals with the influence of environment, genotype, and the combination of both on the expression of the phenotype. First, statistical and biometrical models are constructed. Then statistical methods are explained, and the use of the formulae demonstrated by numerical examples. The cases discussed are simple allelism, multiple allelism and polygenic inheritance. On this basis the next chapter gives the statistical treatment of the interdependence of genetical and environmental factors. Here the method of path coefficients is introduced, and by this method the analysis of correlations and interactions for different degrees of relationship is explained.

The third chapter deals with the same problems, but here they are analysed by means of the analysis of variance for the cases of a hierarchical and a two-way classification (incomplete and complete analysis of variance). The author gives both the method of analysis and the interpretation of the analytical results. The methods apply mainly to animal breeding, but in addition the results are generalised by discussing the special problems which arise in plant breeding and human genetics.

In the fourth chapter the methods given in Chapters 2 and 3 are applied to the special case of artificial selection in respect of one or more characteristics. Here not only the classical designs but also modern methods are considered. The author compares regression analysis, the method of path coefficients and the analysis of variance. Different methods of treatment are also compared with respect to their efficiency and the amount of information they can give.

In all chapters the formulae which are used are derived in a valid manner and the methods of analysis are illustrated by good examples. In several places there are diagrams which help to make the complex connections quite clear. The methods of analysis are clearly illustrated by detailed numerical examples. At the end of the book there is an extensive list of literature, which not only contains the papers mentioned in the text, but is in fact a bibliography on all the questions raised in the course of the discussions. In this way it is easy for the reader to find references in his own field of work on special questions which are not given a place in the book. The last pages give, besides the index and a list of authors, three very instructive tables. Their two-way classification according to problems and methods makes it possible to see the connections between the chapters and to locate the questions which are discussed under different topics from different points of view.

The reader who knows enough in advance to follow the author and who has enough energy to work through nearly 400 pages, will benefit greatly from this book.

18 LI, C. C. **Numbers from Experiments.**—A basic Analysis of Variation. Pittsburgh: The Boxwood Press 1959. pp. 1x + 106, Cloth $4.00, paper $2.75.

G. H. JOWETT, *University of Melbourne, Australia.*

This book is mainly concerned with explaining the algebra involved in the analysis of variance applied to one-way, hierarchical and two-way classifications, and to linear regression.

The author is clearly fascinated by the partitioning of sums of squares and goes to considerable trouble to show how this happens. He makes considerable use of an interesting diagrammatic representation of a comparison between sums of squares

as a comparison between areas made up of actual geometrical squares, which is apparently his own invention.

Summation and suffix notations are used freely, particularly in later chapters, and matrices and orthogonal contrasts are also used, but only to demonstrate the splitting up of a sum of squares in an alternative manner. No basic statistical theory is given, nor is any serious attempt made to explain other aspects of the mathematical statistics. Some space is devoted to establishing expectations of mean squares, but this is based on quoted theorems of the type,

$$E(y_1 + y_2 + \cdots) = E(y_1) + E(y_2) + \cdots ,$$

$$E(y_1 y_2) = \mu^2 \qquad (y_1 , y_2 \quad \text{independent}),$$

the plausibility of which is justified mainly by reference to a very special case where y can take each value with equal probability. An attempt is also made to demonstrate the concept of a linear model; an ingenious example—"Grandma's birthday party"—is used for this purpose, deviations from observed means being interpreted as gains and losses in a poker game by the grandchildren, the money being provided by Grandma with some interference by Grandpa. Illustrative examples used in the exposition are deliberately artificial, being chosen to employ simple numbers and thus concentrate attention on relationships and procedure rather than to suggest applications.

Since the book does not cover the meaning and application of the techniques, it gives little help to anyone seeking to design or interpret the analysis of an experiment. On the other hand, it is not a suitable introduction to analysis of variance for a student of mathematical statistics or statistical method; it is loose and evasive about such important matters as degrees of freedom, testing hypotheses and independence, brings in sophisticated and inadequately explained jargon, and makes vague and unhelpful references to advanced mathematical topics (e.g. the rank of quadratic forms) in cases where the author has not been able to think of simple explanations. However, there is material here and there which, selected with discrimination, could give a teacher ideas for presentation or just tilt the balance of understanding for a student having difficulty with the algebra of the technique.

THE BIOMETRIC SOCIETY

MEETINGS OF E. N. A. R.

Annual Meeting, 1961

The annual meeting of the Eastern North American Region of the Biometrics Society is being held during the meetings of the American Statistical Association at the Roosevelt Hotel in New York City, December 27–30, 1961. Jointly with the Biometrics Section of A. S. A., ten sessions of invited papers and one session of contributed papers have been arranged.

Spring Meeting, 1962

E. N. A. R. will meet jointly with the Institute of Mathematical Statistics at the University of North Carolina, Chapel, Hill, April 12–14, 1962. M. E. Turner, Division of Biometry, Medical College of Viginia, and A. F. Bartholomay, Biophysics Laboratory, Harvard Medical School, Cambridge, are co-chairmen of the E. N. A. R. program committee. H. B. Wells, Department of Biostatistics, University of North Carolina, Chapel Hill is handling local arrangements for E. N. A. R.

Titles for contributed papers should be sent to M. E. Turner, who will then supply authors with abstract forms and appropriate instructions.

Annual Meeting, 1962

The annual meeting of E. N. A. R. in 1962 will be held during the meetings of the American Statistical Association at the Hotel Leamington in Minneapolis, September 7–10, 1962. Joint sessions with the Biometrics Section of A. S. A. are being arranged.

W. N. A. R.

MINUTES OF THE 1961 WNAR BUSINESS MEETING

The annual meeting of WNAR, Biometrics Society was held at 2:30 P. M. June 16, 1961 at the University of Washington, Seattle. William F. Taylor, President, WNAR, presided.

The Secretary's and Treasurer's reports were read and approved. The WNAR student award (consisting of a free year's subscription to *Biometrics*) was discussed at length and a motion was passed providing that any graduate student with a dual interest in the biological sciences and statistics should be considered eligible for the award.

A possible meeting with the AAAS at Denver December 26–31 was discussed and the general concensus of opinion was that we should participate in this meeting.

A motion was passed unanimously that WNAR meet for our annual meeting with AIBS at Oregon State University, Corvallis during the last week of August, 1962.

The nominating committee gave their report and nominations were made from the floor. Those nominated were: for President, Carl A. Bennett, for the two Regional Committee vacancies, Gordon E. Dickerson, Charles Mode, Henry Tucker and Alvin Wiggins.

The meeting adjourned at 3:20 P.M. Present at the meeting: Becker, Bennett,

G., Bennett, C., Berry, Bohidar, Brown, Calvin, Chapman, Hopkins, Leitch, Mantel, Nash, Petersen, Puri, Russell, Sandomire, Taylor, Tucker, Vaughan, Wiggins.

WNAR ELECTION RESULTS

Carl A. Bennett was elected WNAR President for 1962–63 and Charles J. Mode and Henry Tucker were elected to the Regional Committee for 1962–64.

JOINT MEETING OF WNAR AND AAAS

The Western North American Region will meet with the American Association for the Advancement of Science in Denver on December 28, 1961. There will be three sessions entitled "Experimental Design," "Estimation of Populations (mobile and others)," and a "Contributed Papers Session." Members wishing to present papers should contact Dr. Franklin A. Graybill, Statistical Laboratory, Colorado State University, Fort Collins, Colorado, Program Chairman.

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NEWS AND ANNOUNCEMENTS

Members are invited to transmit to their National or Regional Secretary (if members at large, to the General Secretary) news of appointments, distinctions, or retirements, and announcements of professional interest.

NEWS ABOUT MEMBERS

Jacob B. Chassan has been appointed statistician for the Research Department of Hoffmann-La Roche, Inc., at Nutley, N. J.

C. Philip Cox, formerly of the N.I.R.D., Shinfield, England, has joined the staff of the Statistical Laboratory and Department of Statistics, Iowa State University, as Associate Professor. Professor Cox will be teaching and conducting research in the area of biological statistics.

Seymour Geisser has been recently appointed Chief of Biometry of the National Institute of Arthritis and Metabolic Diseases.

Dewey L. Harris, has been appointed as Assistant Professor to the staff of the Statistical Laboratory and Department of Statistics, Iowa State University. Dr. Harris will be consulting, teaching and doing research in the area of Genetics Statistics.

Donald H. Hazelwood, formerly NIH Fellow, Department of Zoology, Washington State University has taken a position as Assistant Professor of Zoology, University of Missouri.

Donald K. Hotchkiss, has been appointed as Assistant Professor to the staff of the Statistical Laboratory and Department of Statistics, Iowa State University. Dr. Hotchkiss will be consulting, teaching, and doing research in the area of statistics applied to animal nutrition.

Robert Macey is now Assistant Professor, Department of Physiology, University of California, Berkeley, moving from the University of Illinois School of Medicine.

J. N. K. Rao of the Statistical Laboratory, and Department of Statistics, Iowa State University, has been promoted to rank of Assistant Professor. Dr. Rao will be teaching and conducting research in survey sampling in his new assignment.

Elmer E. Remmenga, Chief, Computing Center, Colorado State University, will be on sabbatical leave from July, 1961 to July, 1962.

Patrick K. Tomlinson has recently become an Aquatic Biologist, Ocean Salmon Investigation, California Department of Fish and Game. He formerly was in the Biostatistics Section.

Richard W. Vail, Jr. has taken a position as statistician in the Aerospace Corporation, Florida. He previously was statistician for Aerojet General Corporation, Azusa, California.

Pearl A. Van Natta, formerly Biometrician at the Child Research Council, Denver, Colorado, is a self employed statistical consultant.

SOUTHERN METHODIST UNIVERSITY—NEW PROGRAM IN STATISTICS

Southern Methodist University announces the opening of a new Department of Mathematical and Experimental Statistics and Statistical Laboratory in the

Graduate School. Faculty members include Drs. Paul D. Minton and Vanamamalai Seshadri, assisted part-time by Mr. Del West and Mr. Mack Usher.

Coursework leading to the degree of Master of Science will be offered, including courses in mathematical statistics, experimental statistics, probability, sampling theory and design of experiments.

Departmental assistantships are available.

For further information, write to Dr. Paul D. Minton, Department of Mathematical and Experimental Statistics, Southern Methodist University, Dallas 22, Texas.

FLORIDA STATE UNIVERSITY—EXPANDED PROGRAM IN STATISTICS

Beginning in September 1962, the Department of Statistics at the Florida State University will expand its graduate program to study and research leading to the Doctor of Philosophy degree in statistics. The success of the present program, currently limited to study to the Master of Science degree in statistics, has led to the approval of the new advanced training. The curriculum will be modified and expanded to include advanced work in statistical inference and decision theory, stochastic processes, advanced probability, multivariate analysis, operations research, special topics in biometry, theory of general linear hypotheses, non-parametric statistics and sequential analysis. Advanced courses will be offered in alternate years. The program leading to the Master of Science degree will be modified to permit both the thesis and non-thesis types of programs.

The new program will be assisted through the recent addition to the staff of Dr. Vincent Hodgson from the London School of Economics and Political Science. Dr. Hodgson joints Drs. Ralph A. Bradley, Frank Wilcoxon, Richard G. Cornell and S. K. Katti in the Department of Statistics. Additional faculty appointments within the next two years are anticipated.

Facilities have been greatly improved through completion of a new mathematical sciences building in which instructional, laboratory and office space was designed for use of the faculty and graduate students in statistics. The new building also houses an IBM 709 computer for research use.

The Department has a limited number of teaching and research assistantships available. Proposals for three-year graduate fellowships are pending and such fellowships should be available for graduate students entering the new program in September. Interested students are invited to write to Dr. R. A. Bradley, Department of Statistics, the Florida State University, Tallahassee, Florida for further information.

CORRECTIONS

Chin Long Chiang [1960]. A Stochastic Study of the Life Table and Its Applications: I. Probability Distributions of the Biometric Functions. *Biometrics 16*, 618–35.

In formula (2), page 621, for 1_x read l_x. In formula (9), page 622, n should be deleted.

Chin Long Chiang [1961]. A Stochastic Study of the Life Table and Its Applications: III. The Follow-up Study with the Consideration of Competing Risks. *Biometrics 17*, 57–78.

In line 1, page 62, m should be replaced by n. In formula (21), page 66, for $S^2_{\bullet\alpha}$ read $S^2_{\delta\alpha}$. In formula (32), page 69, for $Q_{zk\ 12}$ read $Q_{zk.12}$. In formulas (57) and (58), page 73, the super 2 should be deleted from σ^2. In formula (58), page 73, for Λ_{zk} read Λ_{kk}. In column (2) of table 4, page 77, for 835.87 read 935.87. In line 5 from the bottom, page 77, for $\hat{Q}_{zk}$ read $\hat{q}_{zk}$.

J. K. Abraham [1960]. 154 Note: On an Alternative Method of Computing Tukey's Statistic for the Latin Square Model. *Biometrics 16*, 686–691.

In Table 3, cn^4 should multiply each $\sum^i$, $\sum^j$ and $\sum^k$ appearing, and in Table 4, beneath "Treatments", $\sum^k$ should be similarly corrected.

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by James Maxwell Little, Bowman Gray School of Medicine, Wake Forest College, 1961, 88 pages, $3.00.

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Tome I, N° 3–4 *Juillet-Octobre, 1960*

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Tome II, N° 1 *Mars, 1961*

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Vol. 3, No. 3 August, 1961

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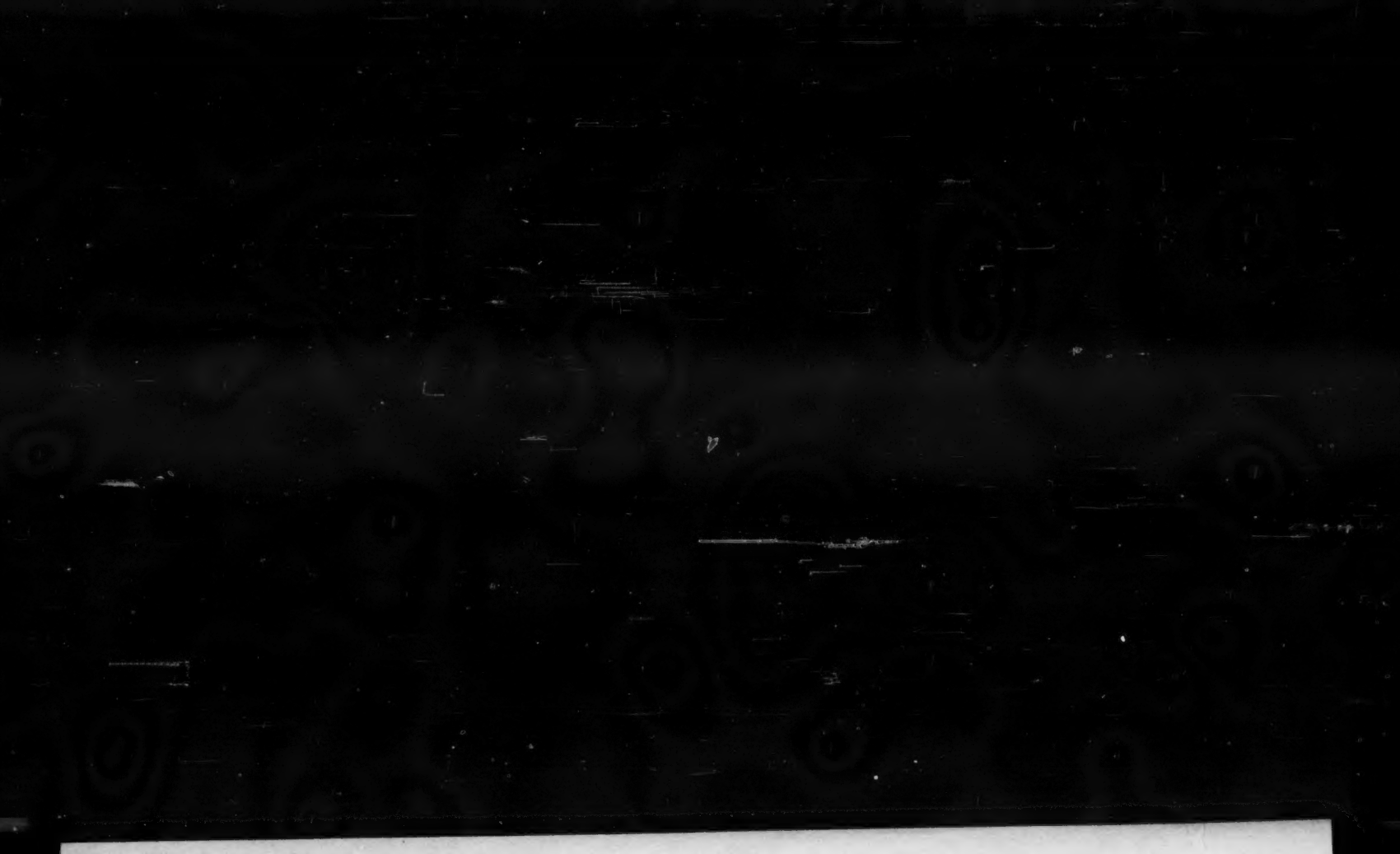
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